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Attorney Docket P1713R1  
PATENT

BOX SER

## CERTIFICATION UNDER 37 CFR 1.10

EM 141 796 365 US: Express Mail Number

June 30, 2000: Date of Deposit

I hereby certify that this Non-provisional Application Transmittal and the documents referred to as enclosed therein are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Assistant Commissioner of Patents, Washington, D.C. 20231.

*Pamela Gavette*  
Pamela Gavette

JC855 U.S. PTO  
09/609721  
06/30/00

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

BOX PATENT APPLICATION  
Assistant Commissioner of Patents  
Washington, D.C. 20231

**NON-PROVISIONAL APPLICATION TRANSMITTAL UNDER 37 CFR 1.53(b)**

Transmitted herewith for filing is a non-provisional patent application:

Inventor(s) (or Application "Identifier"):

**Mark S. Dennis, San Carlos, California**Title: **COMPOUNDS THAT BIND HER2****1. Type of Application**

- ☐ This application is for an original, non-provisional application.
- ☒ This is a non-provisional application claiming priority to provisional application no. 60/142,232, filed 2 July 1999, the entire disclosure of which is hereby incorporated by reference.
- ☐ This is a ☐ continuation-in-part ☐ continuation ☐ divisional application claiming priority to application Serial Number \_\_, filed \_\_, the entire disclosure of which is hereby incorporated by reference.

**2. Papers Enclosed Which Are Required For Filing Date Under 37 CFR 1.53(b) (Non-provisional )**

86 pages of specification  
9 pages of claims  
1 page(s) of abstract  
18 sheet(s) of drawings  
☐ formal ☒ informal

JC855 U.S. PTO  
06/30/00

09/609721-06/30/00

48 page(s) of Sequence Listing

### 3. Declaration or Oath

**(for new and CIP applications; also for Cont./Div. where inventor(s) are being added)**

X An executed declaration of the inventor(s) [x] is enclosed ☐ will follow.

**(for Cont./Div. where inventorship is the same or inventor(s) being deleted)**

— A copy of the executed declaration/oath filed in the prior application is enclosed (37 CFR 1.63(d)).

**(for Cont./Div. where inventor(s) being deleted)**

— A signed statement is attached deleting inventor(s) named in the prior application (see 37 CFR 1.63(d)(2) and 1.33(b)).

#### 4. Assignment

**(for new and CIP applications)**

  x   An Assignment of the invention to GENENTECH, INC. [ ] is enclosed with attached Recordation Form Cover Sheet [x] will follow.

**(for cont./div.)**

\_\_\_\_ The prior application is assigned of record to Genentech, Inc.

**5. Amendments (for continuation and divisional applications)**

\_\_\_\_\_ Cancel in this application original claims \_\_ of the prior application before calculating the filing fee. (At least one original independent claim must be retained for filing purposes.)

\_\_\_\_\_ A preliminary amendment is enclosed. (Claims added by this amendment have been properly numbered consecutively beginning with the number next following the highest numbered original claim in the prior application.)

**Relate Back -- 35 U.S.C. 120 or 35 U.S.C. 119**

\_\_\_\_\_ Amend the specification by inserting before the first line the sentence:

--This is a

\_\_\_\_\_ non-provisional application

continuation

divisional

continuation-in-part

of co-pending application(s)

\_\_\_\_ Serial No. \_\_\_\_ filed on \_\_\_\_, which application(s) is(are) incorporated herein by reference and to

\_\_\_\_ International Application \_ filed on \_\_ which designated the U.S., which application(s) is(are) incorporated herein by reference and to which application(s) priority is claimed under 35 USC §120.--

\_\_\_\_\_ provisional application No. \_ filed \_\_, the entire disclosure of which is hereby incorporated by reference and to which application(s) priority is claimed under 35 USC §119.--.

The fee has been calculated as follows:

CLAIMS FOR FEE CALCULATION					
Number Filed		Number Extra		Rate	Basic Fee 37 CFR 1.16(a) \$690.00
Total Claims	38	- 20 =	18	X \$18.00	\$342.00
Independent Claims	1	- 3 =	0	X \$78.00	\$0.00
<u>X</u> Multiple dependent claim(s), if any				+ \$260.00	\$260.00
<b>Filing Fee Calculation</b>					<b>\$1,292.00</b>

The Commissioner is hereby authorized to charge Deposit Account No. 07-0630 in the amount of \$1,292.00.00. **A duplicate copy of this transmittal is enclosed.**

The Commissioner is hereby authorized to charge any additional fees required under 37 CFR §1.16 and 1.17, or credit overpayment to Deposit Account No. 07-0630. **A duplicate copy of this sheet is enclosed.**

☐ Information Disclosure Statement (37 CFR §1.98) w/ PTO-1449 and citations

☒ Submission of "Sequence Listing", computer readable copy, certificate re: sequence listing, and/or amendment pertaining thereto for biological invention containing nucleotide and/or amino acid sequence.

☐ A new Power of Attorney or authorization of agent.

☐ Other:

***[This item must be completed and the necessary papers filed in the prior application if the period set in the prior application has run]***

\_\_\_\_\_ A petition, fee and/or response has been filed to extend the term in the pending prior application until \_\_\_\_\_

**11. Correspondence Address:**

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## COMPOUNDS THAT BIND HER2

### Background of the Invention

#### 10 Related Applications

This application is a non-provisional application filed under 37 CFR 1.53(b)(1), claiming priority under 35 USC 119(e) to provisional application number 60\142,232 filed July 2, 1999, the contents of which are incorporated herein by reference.

15

#### Field of the Invention

20 This invention relates to novel compounds which bind to the human erbB2 gene product (ErbB2, also known as HER2, or c-ErbB-2). In particular aspects, the invention relates to the treatment of disorders characterized by the expression of ErbB2 utilizing the novel compounds of the invention. The invention also relates to compositions, such as pharmaceutical compositions, comprising the novel compounds, as well as their use in research, diagnostic, therapeutic, and prophylactic methods.

25

#### Description of Related Disclosures

30 Phage display provides a means for generating peptides and protein variants through randomization of specific amino acid residues within a template sequence or by generation of naive peptide libraries (Lowman, H. (1998) Methods Mol. Biol. 87:249-264; Lowman (1997) Annu. Rev. Biophys. Biomol. Struct. 26:401-424). Identification and isolation of displayed proteins or peptides that bind a predetermined target molecule can be

achieved through enrichment of displaying phage over non-binding or weakly binding variants on immobilized target molecules (Lowman, H. (1989), supra). Successive rounds of mutagenesis and selection can yield peptide ligands or protein variants with high affinity for cellular receptors (Lowman, H. (1998), supra). The technique has been used to identify peptide motifs that home to, for example, a cellular target (Arap et al., (1998) Science 279:377-380), or to generate affinity improved or matured peptide ligands from native protein binding ligands (Lowman et al., (1991) Biochemistry 30: 10832-10838). Examples of affinity or specificity improved proteins include human growth hormone, zinc fingers, protease inhibitors, atrial natriuretic peptides, and antibodies (Wells, J. and Lowman H. (1992) Curr. Opin. Struct. Biol. 2:597-604; Clackson, T. and Wells, J. (1994) Trends Biotechnol. 12:173-184; Lowman et al., (1991) Biochemistry 30(10):832-838; Lowman et al. and Wells J. (1993) J. Mol. Biol. 234:564-578; Dennis M. and Lazarus R. (1994) J Biol. Chem. 269(22):137-144).

Utilizing *in vivo* phage selection, phage display has been used to identify and isolate peptides capable of mediating selective localization to various organs such as brain and kidney (Pasqualini and Ruoslohti (1996) Nature 380:364-366) as well as to identify peptides that home to particular tumor types bearing  $\alpha_v\beta_3$  or  $\alpha_v\beta_5$  integrins (Arap et al., (1998) Science 279:377-380). U.S. Patent 5,627,263 describes peptides that are recognized by and selectively bind the  $\alpha_5\beta_1$  integrin. Using structurally constrained peptide libraries generated by monovalent phage display, 14 amino acid peptides that specifically bind to insulin-like growth factor 1 binding proteins (IGFBPs) have been isolated (Lowman et al., (1998) Biochemistry, 37:8870-8878). The

peptides contain a helix structure and bind IGFBPs in vitro liberating insulin like growth factor- $\alpha$  (IGF-1) activity (Lowman et al., (1998) supra).

Particular cellular receptors and their ligands, especially those implicated in the pathogenesis of various human malignancies, have recently been the focus of much attention in the scientific community as novel protein based therapeutics enter the clinic. For example, it has been found that the human erbB2 gene (also known as her2, or c-erbB-2), which encodes a 185-kd transmembrane glycoprotein receptor (p185<sup>HER2</sup>) related to the epidermal growth factor receptor (EGFR), is overexpressed in about 25% to 30% of human breast cancer (Slamon et al., (1987) Science 235:177-182; Slamon et al., (1989) Science 244:707-712). Several lines of evidence support a direct role for ErbB2 in the pathogenesis and clinical aggressiveness of ErbB2-overexpressing tumors. The introduction of erbB2 into non-neoplastic cells has been shown to cause their malignant transformation (Hudziak et al., (1987) Proc. Natl. Acad. Sci. USA 84:7159-7163; DiFiore et al., (1987) Science 237:78-182). Transgenic mice that express HER2 were found to develop mammary tumors (Guy et al., (1992) Proc. Natl. Acad. Sci. USA 89:10578-10582).

ErbB2 overexpression is commonly regarded as a predictor of a poor prognosis, especially in patients with primary disease that involves axillary lymph nodes (Slamon et al., (1987) and (1989), supra; Ravdin and Chamness, (1995) Gene 159:19-27; and Hynes and Stern, (1994) Biochim. Biophys. Acta 1198:165-184). Overexpression has also been linked to sensitivity and/or resistance to hormone therapy and chemotherapeutic regimens, including CMF (cyclophosphamide, methotrexate, and fluoruracil) and anthracyclines (Baselga et al., (1997) Oncology 11(3 Suppl

1):43-48).

A recombinant humanized anti-ErbB2 monoclonal antibody (a humanized version of the murine anti-ErbB2 antibody 4D5, referred to as rhuMAb HER2 or HERCEPTIN®) is therapeutically active in patients with ErbB2-overexpressing metastatic breast cancers that have previously received extensive anti-cancer therapy (Baselga et al., (1996) J. Clin. Oncol. 14:737-744).

### Summary of the Invention

The present invention provides compounds which bind to the human erbB2 gene product (ErbB2). The compounds of the present invention (referred to as peptide ligands herein) are, for example, peptides or peptide derivatives such as peptide mimetics and peptide analogs. Preferred peptide ligands include linear and cyclic peptides, preferably cyclic peptide compounds comprising the following core formula:

-Cys-Xaa-Xaa-Xaa-Xaa-Cys-

and preferably those having the general formula:

Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Cys-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys (SEQ ID NO:70)

or the general formula:

Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa, including dimers and other combinations of the foregoing general structures. Preferred among the peptide ligands of the invention are peptides comprising the core formula:

-Cys-Cys/Ile-Gly-Pro-Gly-Cys- (SEQ ID NO:71)

Specific examples of such compounds include cyclic peptides of between about 10 and 60 amino acid residues and optionally including N- or C-terminal modifications or both, such as esters,

amides, salts and other derivatives thereof. According to preferred aspects of the invention, the compounds are preferably non-naturally occurring amino acid sequences that bind ErbB2. Preferably the compound is a non-naturally occurring amino acid sequence of between about 5 and about 50 amino acid residues. Preferred compounds are cyclic peptides having the foregoing general formulae and having of between about 20 and about 30 amino acid residues and include dimers and other combinations thereof.

In particular aspects the invention is directed to combinations of peptide ligands with other peptide ligands or with other proteins, especially serum proteins or peptides. The combinations are prepared with various objectives in mind, including; increasing the affinity or avidity of the peptide ligand for its target molecule, as for example, by use of various multimerization domains; increasing the stability of the peptide ligand or facilitating its recovery and purification, as for example by expressing the peptide ligand as a Z protein fusion; improving the therapeutic efficacy of the peptide ligand in aspects of the invention involving *in vivo* use of the peptide ligand, by for example, increasing or decreasing the serum half life, by for example, fusing the peptide ligand to a plasma protein such as serum albumin, an immunoglobulin, apolipoproteins or transferrin (such fusion being made conveniently in recombinant host cells or by the use of bifunctional crosslinking agents) and introducing additional functionalities, as for example, those of a functional Fc domain or cytotoxic or enzyme moiety.

According to a preferred aspect of the present invention the compound of the invention is linked to a multimerization domain.

The multimerization domain is preferably an immunoglobulin sequence or, for example, a leucine zipper sequence. According to this aspect of the invention the immunoglobulin sequence is preferably an immunoglobulin constant region sequence and especially the constant region of an immunoglobulin heavy chain. According to preferred aspects of the invention, the multimerization domain pairs with one or more companion multimerization domains to provide homo- and hetero-multimer compositions. Preferred according to this aspect of the present invention are homo- and hetero-multimers, especially homo- and heterodimers wherein the multimerization domains are immunoglobulin heavy chain constant regions which pair to provide functional immunoglobulin Fc domains. Therefore, according to preferred aspects, the invention provides a hybrid molecule comprising a compound of the invention which functions to target an ErbB2 bearing cell type and functional immunoglobulin Fc domain possessing an effector function associated with a functional immunoglobulin Fc domain.

Hybrid molecules according to this aspect of the invention optionally include a further functional moiety such as an enzyme moiety or a cytotoxic moiety. For example, the additional functional domain may be an enzyme covalently linked to a hybrid molecule and capable of acting on a prodrug in such a way as to convert the prodrug to its more active form. The optional functional domain, according to certain preferred aspects of the invention, may be a cytotoxic agent linked by, for example, covalent attachment, to a hybrid molecule. Preferred cytotoxic agents include, for example, chemotherapeutic agents, toxins and radioactive isotopes. The compounds including the hybrid molecules and compositions comprising them are used in binding or

detecting the human erbB2 gene product and optionally delivering a functional moiety such as an enzyme or cytotoxic drug to an ErbB2 bearing cell type.

5 In one embodiment, the compound of the present invention, such as the hybrid molecule described above, is a polypeptide and the invention encompasses a composition of matter comprising an isolated nucleic acid, preferably DNA, encoding the polypeptide of the invention. According to this aspect, the invention further comprises an expression control sequence operably linked to the DNA molecule, an expression vector, preferably a plasmid, comprising the DNA molecule, where the control sequence is recognized by a host cell transformed with the vector, and a host cell transformed with the vector. According to preferred aspects the nucleic acid encodes a hybrid molecule comprising a peptide compound of the invention and an immunoglobulin constant region domain sequence. The nucleic acid molecule according to this aspect of the present invention encodes a hybrid molecule and the nucleic acid encoding the peptide compound of the invention is operably linked to (in the sense that the DNA sequences are contiguous and in reading frame) the immunoglobulin domain sequence. Optionally the DNA sequences may be linked through a nucleic acid sequence encoding an optional linker domain amino acid sequence.

25 The compositions of the present invention may be made by a process which includes the steps of isolating or synthesizing nucleic acid sequences encoding any of the amino acid sequences of the invention, ligating the nucleic acid sequence into a suitable expression vector capable of expressing the nucleic acid sequence in a suitable host, transforming the host with the expression vector into which the nucleic acid sequence has been

ligated, and culturing the host under conditions suitable for expression of the nucleic acid sequence, whereby the protein encoded by the selected nucleic acid sequence is expressed by the host. Preferably, the polypeptide is then recovered from the host cell culture. In this process, the ligating step may further contemplate ligating the nucleic acid into a suitable expression vector such that the nucleic acid is operably linked to a suitable secretory signal, whereby the amino acid sequence is secreted by the host.

The invention includes compositions, including pharmaceutical compositions, comprising the compounds of the invention, especially for the detection and treatment of diseases or disorders associated with erbB2 gene expression. Provided are, for example, kits and articles of manufacture for the detection and treatment of cancer. Kits and articles of manufacture preferably include:

- (a) a container;
- (b) a label on or associated with said container; and
- (c) a composition comprising a compound of the present invention contained within said container wherein, according to certain embodiments, the composition is effective for treating a disease or disorder associated with erbB2 gene expression, such as cancer. Preferably, the label on said container indicates that the composition can be used for treating cancer, and the compound in said composition comprises a compound as described herein which binds to the human erbB2 gene product. The kits optionally include accessory components such as a second container comprising a pharmaceutically-acceptable buffer and instructions for using the composition to treat a disorder.

Also disclosed are methods useful in the treatment of



various diseases and disorders, such as cancer, especially those characterized by the involvement of ErbB2. Therefore, the invention provides a method of treating an ErbB2 mediated or associated disease or disorder in a host in need thereof

5 comprising administering to the host a therapeutically effective amount of a compound of the invention. The present invention further provides various dosage forms of the compounds of the present invention, including but not limited to, those suitable for parenteral, oral, rectal and pulmonary administration of a  
10 compound. In preferred aspects of the present invention, a therapeutic dosage form is provided suitable for intravenous delivery and the invention provides for the treatment of diseases or disorders involving a ErbB2 mediated or associated process or event such as cancer.

#### **Brief Description of the Drawings**

Figure 1 is a schematic representation of a native IgG and fragments thereof resulting from papain and pepsin digest. Disulfide bonds are represented by -S-S- between, for example, the CH1 and CL domains. In the figure, V is variable domain; C is constant domain; L stands for light chain and H stands for heavy chain.

Figure 2A depicts alignments of native IgG Fc region amino acid sequences. Shown are human (hum) IgG Fc region sequences, humIgG1 (non-A and A allotypes) (SEQ ID NOs:72 and 73 ,  
25 respectively), humIgG2 (SEQ ID NO:74), humIgG3 (SEQ ID NO:75) and humIgG4 (SEQ ID NO:76), are shown. The human IgG1 sequence is the non-A allotype, and differences between this sequence and the A allotype (at positions 356 and 358; EU numbering system) are  
30 shown below the human IgG1 sequence. Also shown are native

murine (mur) IgG Fc region sequences, murIgG1 (SEQ ID NO:77), murIgG2A (SEQ ID NO:78), murIgG2B (SEQ ID NO:79) and murIgG3 (SEQ ID NO:80), are also shown. Figure 2B shows the percent identity among the Fc region sequences of Figure 2A.

5 Figure 3 shows the alignments of native human IgG Fc region sequences, humIgG1 (non-A and A allotypes) (SEQ ID NOs:72 and 73), humIgG2 (SEQ ID NO:74), humIgG3 (SEQ ID NO:75) and humIgG4 (SEQ ID NO:76) with differences between the sequences marked with asterisks.

10 Figure 4 shows the enrichment of polyvalent peptide phage that bind the HER2 extracellular domain (ECD). The ratio of phage eluted from a well coated with HER2 versus a well coated with BSA is shown for rounds 3 and 4 of selection.

15 Figure 5 shows the results of a phage binding assay. Phage clones 1.1, 5.1 and 7.1 were found to bind immobilized HER2-ECD, but not BSA or closely related HER3 or HER4 indicating they specifically recognized HER2-ECD.

Figure 6 shows EC50 determination for peptide 1.1.FIZb binding immobilized HER2.

20 Figure 7 shows the results of a competition assay for synthetic peptides HER201 and HER212 as well as recombinant peptides 1.1.FI-Z and 7.1c-Z with peptide 1.1.FI-Zb for binding to immobilized HER2-ECD.

25 Figures 8A-C. Figure 8A shows the 1.1.FI-Z (SEQ ID NO:81) preparation (S) purified using a Superdex 75 into monomer (M) and dimer (D) containing fractions. Figure 8B shows an SDS PAGE analysis of starting material and fractions from the SUPERDEX™ 75 column for peptide 1.1.FI-Z. Figure 8C shows HER2 binding activity coinciding with dimer fractions of 1.1.FI-Z when assayed  
30 using a competition assay.

Figures 9A-C. Figure 9A shows the (1.1FI)<sub>2</sub>-Z (SEQ ID NO:82) (1.1FI repeated twice and fused to the Z domain of protein A) preparation purified using a SUPERDEX™ 75 to monomer and dimer containing fractions. Figure 9B shows and SDS PAGE analysis of fractions from the SUPERDEX™ column for peptide (1.1FI)<sub>2</sub>-Z. Figure 9C shows HER2 binding activity coinciding with monomer fractions of (1.1FI)<sub>2</sub>-Z when assayed using a competition assay.

Figures 10A and B. Figures 10A and 10B show that peptides HER201 and 7.1c-Z block the binding of Class 1 and Class 7 phage suggesting that both classes of peptides bind to the same site on HER2.

Figure 11 shows examples of Class 1 and Class 7 sequences revealing a core homology region between the two classes of peptides. Sequence 7.1c (SEQ ID NO:83), 1.1.2 (SEQ ID NO:84), 1.1.FC (SEQ ID NO:85), 1.1.FA (SEQ ID NO:86), 1.1.FB (SEQ ID NO:87), 1.1.FH (SEQ ID NO:88), 1.1.CF (SEQ ID NO:89).

Figure 12 shows the results of a competition assay of Class 1 and Class 7 peptides with known monoclonal antibodies directed against HER2 for binding HER2-ECD. The peptides do not compete with the monoclonal antibodies for binding HER2-ECD suggesting that the peptides bind a HER2-ECD site distinct from that recognized by known monoclonal antibodies.

Figure 13 shows the results of a binding assay conducted using peptide 1.1.FI-Zb and cells either expressing HER2 at different levels (MDA 361 [4x10<sup>5</sup> receptors/cell]) and BT 474 ([3x10<sup>6</sup> receptors/cell]) or cells not expressing HER2 (BaF3). 1.1.FI-Zb was found to bind cells proportional to the number of HER2 receptors expressed on the cell and concentration of 1.1.FI-Zb peptide.

Figure 14 shows the results of SDS PAGE analysis under

oxidizing and reducing conditions of peptide 1.1.FI fused through a linker to the hinge, CH1 and CH2 domains of human IgG1 (1.1FI-Fc). The molecular weight shift under the two conditions suggests dimerization of the Ig constant regions and the formation of a Fc domain.

Figure 15 shows the deduced peptide sequences from clones in libraries 1.1 and 7.1. Sequence 1.1 (SEQ ID NO:57); 1.1.8 (SEQ ID NO:58); 1.1.9 (SEQ ID NO:59); 1.1.10 (SEQ ID NO:60); 1.1.11 (SEQ ID NO:61); 1.1.2 (SEQ ID NO:62); 1.1.6 (SEQ ID NO:63); 1.1.11 (SEQ ID NO:64); 1.1.3 (SEQ ID NO:65); 1.1.4 (SEQ ID NO:66); 1.1.5 (SEQ ID NO:67); 1.1.7 (SEQ ID NO:68); Consensus (SEQ ID NO:69); 7.1 (SEQ ID NO:45); 7.1.1 (SEQ ID NO:46); 7.1.9 (SEQ ID NO:47); 7.1.6 (SEQ ID NO:48); 7.1.5 (SEQ ID NO:49); 7.1.3 (SEQ ID NO:50); 7.1.4 (SEQ ID NO:51); 7.1.2 (SEQ ID NO:52); 7.1.7 (SEQ ID NO:53); 7.1.8 (SEQ ID NO:54); 7.1.11 (SEQ ID NO:55); Consensus (SEQ ID NO:56).

Figure 16 shows the sequences from random clones for each library by the fourth round of selection. Sequence 1.1 (SEQ ID NO:57); Consensus (SEQ ID NO:58); 1.1.FC (SEQ ID NO:30); 1.1.FN (SEQ ID NO:31); 1.1.FA (SEQ ID NO:1); 1.1.FM (SEQ ID NO:2); 1.1.FE (SEQ ID NO:3); 1.1.FH (SEQ ID NO:29); 1.1.FB (SEQ ID NO:12); 1.1.FF (SEQ ID NO:13); 1.1.FI (SEQ ID NO:14); 1.1.FK (SEQ ID NO:15); 1.1.FD (SEQ ID NO:16); 1.1.FQ (SEQ ID NO:17); 1.1.FS (SEQ ID NO:18); 1.1.FX (SEQ ID NO:9); 1.1.FY (SEQ ID NO:10); 1.1.FZ (SEQ ID NO:11); 1.1.NC (SEQ ID NO:4); 1.1.NB (SEQ ID NO:5); 1.1.NM (SEQ ID NO:6); 1.1.NQ (SEQ ID NO:7); 1.1.NA (SEQ ID NO:19); 1.1.NG (SEQ ID NO:20); 1.1.NH (SEQ ID NO:21); 1.1.NE (SEQ ID NO:22); 1.1.NJ (SEQ ID NO:23); 1.1.NF (SEQ ID NO:24); 1.1.NK (SEQ ID NO:25); 1.1.NR (SEQ ID NO:26); 1.1.CF (SEQ ID NO:28); 1.1.CA (SEQ ID NO:32); 1.1.CB (SEQ ID NO:33); 1.1.CC (SEQ ID

NO:34); 1.1.CD (SEQ ID NO:35); 1.1.CE (SEQ ID NO:36); 1.1.CG (SEQ ID NO:37); 1.1.CH (SEQ ID NO:38); 1.1.CI (SEQ ID NO:39); 1.1.CJ (SEQ ID NO:40); 1.1.CL (SEQ ID NO:41); 1.1.CM (SEQ ID NO:42); 1.1.CP (SEQ ID NO:43).

Figure 17 shows the results of a competition assay of 1.1FI-Fc and 1.1FI-Z with peptide 1.1FI-Zb for binding to immobilized HER2-ECD.

### **Detailed Description of the Preferred Embodiments**

#### **Definitions**

The terms "HER2", "ErbB2" "c-Erb-B2" are used interchangeably. Unless indicated otherwise, the terms "ErbB2" "c-Erb-B2" and "HER2" when used herein refer to the human protein and "her2", "erbB2" and "c-erb-B2" refer to the human gene. The human erbB2 gene and ErbB2 protein are described in, for example, Semba et al., (1985) PNAS (USA) 82:6497-6501 and Yamamoto et al. (1986) Nature 319:230-234 (Genebank accession number X03363). ErbB2 comprises four domains (Domains 1-4).

The term "peptide ligand" within the context of the present invention is meant to refer to amino acid sequences, regardless of their origin, that function to bind ErbB2. Peptide ligands within the context of the present invention are generally constrained (that is, having some element of structure as, for example, the presence of amino acids which initiate a  $\beta$  turn or  $\beta$  pleated sheet, or for example, cyclized by the presence of disulfide bonded Cys residues) or unconstrained (e.g., linear) amino acid sequences of less than about 50 amino acid residues, and preferably less than about 40 amino acid residues. Of the peptide ligands less than about 40 amino acid residues, preferred are the peptide ligands of between about 10 and about 30 amino

acid residues and especially the peptide ligands of about 20 to about 30 amino acid residues. However, upon reading the instant disclosure, the skilled artisan will recognize that it is not the length of a particular peptide ligand but its ability to bind ErbB2 that distinguishes the peptide ligand of the present invention. Therefore, peptide ligands of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 and 30 amino acid residues, for example, are equally likely to be peptide ligands within the context of the present invention.

A peptide ligand of the present invention will bind ErbB2 with sufficient affinity and specificity if the peptide ligand "homes" to, "binds" or "targets" ErbB2, such as an ErbB2 bearing cell, in vitro and preferably in vivo (see, for example, the use of the term "homes to," "homing," and "targets" in Pasqualini and Ruoslahti (1996) Nature, 380:364-366 and Arap et al., (1998) Science 279:377-380). In general, the peptide ligand will bind ErbB2 with an affinity of less than about 1  $\mu$ M, preferably less about 100 nM and more preferably less than about 10 nM as determined by an in vitro assay such as a competition assay utilizing ErbB substrate analogous to those described by Jones et al., (1999) FEBS Letters 447:227-231. However, peptide ligands having an affinity for ErbB2 of less than about 1 nM and preferably between about 1 pM and 1 nM are equally likely to be peptide ligands within the context of the present invention. In general a peptide ligand that binds ErbB2 as described above can be isolated and identified by any of a number of art standard techniques as described herein as for example by binding an immobilized ErbB2 molecule.

As mentioned, peptides ligands are amino acid sequences as

described above which may contain naturally as well as non-naturally occurring amino acid residues. Therefore, so-called "peptide mimetics" and "peptide analogs" which may include non-amino acid chemical structures that mimic the structure of a particular amino acid or peptide may be peptide ligands within the context of the invention. Such mimetics or analogs are characterized generally as exhibiting similar physical characteristics such as size, charge or hydrophobicity present in the appropriate spacial orientation as found in their peptide counterparts. A specific example of peptide mimetic compound is a compound in which the amide bond between one or more of the amino acids is replaced by, for example, a carbon-carbon bond or other bond as is well known in the art (see, for example Sawyer, in Peptide Based Drug Design pp. 378-422 (ACS, Washington DC 1995)).

Therefore, the term "amino acid" within the scope of the present invention is used in its broadest sense and is meant to include naturally occurring L  $\alpha$ -amino acids or residues. The commonly used one and three letter abbreviations for naturally occurring amino acids are used herein (Lehninger, A.L., Biochemistry, 2d ed., pp. 71-92, (1975), Worth Publishers, New York). The term includes D-amino acids as well as chemically modified amino acids such as amino acid analogs, naturally occurring amino acids that are not usually incorporated into proteins such as norleucine, and chemically synthesized compounds having properties known in the art to be characteristic of an amino acid. For example, analogs or mimetics of phenylalanine or proline, which allow the same conformational restriction of the peptide compounds as natural Phe or Pro are included within the definition of amino acid. Such analogs and mimetics are referred

to herein as "functional equivalents" of an amino acid. Other examples of amino acids are listed by Roberts and Vellaccio (The Peptides: Analysis, Synthesis, Biology,) Eds. Gross and Meiehofer, Vol. 5 p 341, Academic Press, Inc, N.Y. 1983, which is incorporated herein by reference.

Peptide ligands synthesized by, for example, standard solid phase synthesis techniques, are not limited to amino acids encoded by genes. Commonly encountered amino acids which are not encoded by the genetic code, include, for example, those described in International Publication No. WO 90/01940 such as, for example, 2-amino adipic acid (Aad) for Glu and Asp; 2-aminopimelic acid (Apm) for Glu and Asp; 2-aminobutyric (Abu) acid for Met, Leu, and other aliphatic amino acids; 2-aminoheptanoic acid (Ahe) for Met, Leu and other aliphatic amino acids; 2-aminoisobutyric acid (Aib) for Gly; cyclohexylalanine (Cha) for Val, and Leu and Ile; homoarginine (Har) for Arg and Lys; 2,3-diaminopropionic acid (Dpr) for Lys, Arg and His; N-ethylglycine (EtGly) for Gly, Pro, and Ala; N-ethylglycine (EtGly) for Gly, Pro, and Ala; N-ethylasparagine (EtAsn) for Asn, and Gln; Hydroxyllysine (Hyl) for Lys; allohydroxyllysine (AHyl) for Lys; 3-(and 4)hydroxyproline (3Hyp, 4Hyp) for Pro, Ser, and Thr; allo-isoleucine (AIle) for Ile, Leu, and Val; p-amidinophenylalanine for Ala; N-methylglycine (MeGly, sarcosine) for Gly, Pro, and Ala; N-methylisoleucine (MeIle) for Ile; Norvaline (Nva) for Met and other aliphatic amino acids; Norleucine (Nle) for Met and other aliphatic amino acids; Ornithine (Orn) for Lys, Arg and His; Citrulline (Cit) and methionine sulfoxide (MSO) for Thr, Asn and Gln; N-methylphenylalanine (MePhe), trimethylphenylalanine, halo (F, Cl, Br, and I)phenylalanine, triflourylphenylalanine, for Phe.



Conservative amino acid substitutions within the context of the invention are shown in Table 1 under the heading of "exemplary substitutions" and "preferred substitutions". If preferred substitutions do not result in a decrease or change in HER2 binding, then more substantial changes, denominated "exemplary substitutions" in Table 1, or as further described herein, may be introduced and the products tested for HER2 binding.

**Table 1**

<b>Original Residue</b>	<b>Exemplary Substitutions</b>	<b>Preferred Substitutions</b>
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; asp, lys; arg	gln
Asp (D)	glu; asn	glu
Cys (C)	ser; ala	ser
Gln (Q)	asn; glu	asn
Glu (E)	asp; gln	asp
Gly (G)	ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu

Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	tyr
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

Peptide ligands within the context of the present invention are preferably non-naturally occurring amino acid sequences. By non-naturally occurring is meant that the amino acid sequence of the particular peptide ligand is not found in nature. According to the present invention the term "non-naturally occurring" is used to refer to a peptide ligand that corresponds to a non-native or non-naturally occurring amino acid sequence. Peptide ligands of this variety may be produced or selected using a variety of techniques well known to the skilled artisan. For example, constrained or unconstrained peptide libraries may be randomly generated and displayed on phage utilizing art standard techniques (for example, Lowman et al., (1998) Biochemistry

37:8870-8878).

At least three distinct species of peptide ligands can be distinguished based upon function associated with binding ErbB2. They will be referred to herein as "neutral," "agonist" and "antagonist" peptide ligands. In general, a neutral peptide ligand functions to bind ErbB2 as described above. Neutral peptide ligands are preferred in aspects of the present invention where targeting of a particular cell type bearing ErbB2 with, for example, a cytotoxic agent or an enzyme is desired.

In general, an "agonist" peptide ligand in addition to binding ErbB2, has a direct effect on an ErbB2 bearing cell. Preferably the agonist peptide ligand will bind ErbB2 as described and, as well, initiate or mediate an event associated with the ErbB2-ErbB3 protein complex and/or the ErbB2-ErbB4 protein complex such as, for example, the ability to cause the intracellular kinase domain to phosphorylate tyrosine residues in the ErbB2 receptor complex. Additionally, binding of the agonist peptide ligand maybe associated with dimerization of the ErbB2 receptor. The ability to induce ErbB2 receptor mediated phosphorylation or ErbB2 receptor dimerization can be quantified using art standard techniques such as tyrosine phosphorylation assays and SDS PAGE.

By contrast, an "antagonist" peptide ligand acts to reduce the activity associated with a natural ligand binding the ErbB2-ErbB3 protein complex and/or ErbB2-ErbB4 protein complex, for example, the cellular response induced by the binding of the native ligand, by for example, binding to and blocking the association of ErbB2-ErbB3 protein complex and/or ErbB2-ErbB4 protein complex with a native or naturally occurring ligand.

However, the foregoing classes are not limiting. For

example, in certain embodiments, binding of a peptide ligand causes internalization of the ErbB2 receptor, or the induction of associated cellular events such as the induction of programmed cell death or apoptosis. Peptide ligands that initiate internalization of ErbB2 or an ErbB2 receptor complex are especially useful in embodiments of the invention requiring intracellular delivery of a cytotoxic agent as described herein below.

The phrase "induces apoptosis" or "capable of inducing apoptosis" refers to the ability of a compound to induce programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). The cell is one which expresses or overexpresses the ErbB2 receptor. Preferably the "cell" is a tumor cell, e.g. a breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, thyroid, pancreatic or bladder cell. In vitro, the cell may be a SKBR3, BT474, Calu 3 cell, MDA-MB-453, MDA-MB-361 or SKOV3 cell. Various methods are available for evaluating the cellular events associated with apoptosis. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the compound which induces apoptosis is one which results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay using BT474 cells.

"Heregulin" (HRG) when used herein refers to a polypeptide which activates the ErbB2-ErbB3 and ErbB2-ErbB4 protein complexes (*i.e.* induces phosphorylation of tyrosine residues in the complex upon binding thereto). Various polypeptides encompassed by this term are disclosed in Jones et al., (1999) FEBS Letters 447:227-231; Holmes et al., (1992) Science, 256:1205-1210; WO 92/20798; Wen et al., (1994) Mol. Cell. Biol., 14(3):1909-1919; and Marchionni et al., (1993) Nature, 362:312-318, for example. The term includes biologically active fragments and/or variants of a naturally occurring HRG polypeptide, such as an EGF-like domain fragment thereof (e.g. HRG $\beta$ <sub>177-244</sub>).

The "ErbB2-ErbB3 protein complex" and "ErbB2-ErbB4 protein complex" are noncovalently associated oligomers of the ErbB2 receptor and the ErbB3 receptor or ErbB4 receptor, respectively. The complexes form on a cell expressing both of these receptors and can be isolated by immunoprecipitation and analyzed by SDS-PAGE as described in Sliwkowski et al., (1994) J. Biol. Chem., 269(20):14661-14665.

The term "multimerization domain" as used in particular aspects of the present invention, is meant to refer to the portion of the molecule to which the peptide ligand is joined, either directly or through a "linker domain." The multimerization domain is an amino acid domain which, according to preferred embodiments, facilitates the interaction of two or more multimerization domains. While the multimerization domain promotes the interaction between two or more multimerization domains, there is no requirement within the context of the present invention that the peptide ligand joined to a multimerization domain be present as a portion of a multimer.

According to preferred aspects of the present invention the

multimerization domain is a polypeptide which promotes the stable interaction of two or more multimerization domains. By way of example and not limitation, a multimerization domain may be an immunoglobulin sequence, such as an immunoglobulin constant region, a leucine zipper, a hydrophobic region, a hydrophilic region, a polypeptide comprising a free thiol which forms an intermolecular disulfide bond between two or more multimerization domains or, for example a "protuberance-into-cavity" domain described in U.S. Patent 5,731,168. In that patent, protuberances are constructed by replacing small amino acid side chains from the interface of a first polypeptide with a larger side chain (for example a tyrosine or tryptophan). Compensatory cavities of identical or similar size to the protuberances are optionally created on the interface of a second polypeptide by replacing large amino acid side chains with smaller ones (for example alanine or threonine).

Therefore, in a preferred aspect, the multimerization domain provides that portion of the molecule which promotes or allows stable interaction of two or more multimerization domains and promotes or allows the formation of dimers and other multimers from monomeric multimerization domains. Preferably, according to this aspect of the invention, multimerization domains are immunoglobulin constant region domains. Immunoglobulin constant domains provide the advantage of improving in vivo circulating half-life of the compounds of the invention and optionally allow the skilled artisan to incorporate an "effector function" as described herein below into certain aspects of the invention.

Throughout the present specification and claims, the numbering of the residues in an immunoglobulin heavy chain is that of the EU index as in Kabat et al., Sequences of Proteins of

Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991), expressly incorporated herein by reference. The "EU index as in Kabat" refers to the residue numbering of the human IgG1 EU antibody.

5 "Antibodies" (Abs) and "immunoglobulins" (Igs) are glycoproteins having the same structural characteristics. While antibodies exhibit binding specificity to a specific antigen, immunoglobulins include both antibodies and other antibody-like molecules which lack antigen specificity. Polypeptides of the latter kind are, for example, produced at low levels by the lymph system and at increased levels by myelomas.

10 "Antibodies" and "immunoglobulins" are usually heterotetrameric glycoproteins of about 150,000 Daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has an amino (N) terminal variable domain (VH) followed by carboxy (C) terminal constant domains. Each light chain has a variable N-terminal domain (VL) and a C-terminal constant domain; the constant domain of the light chain (CL) is aligned with the first constant domain (CH1) of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. According to the domain definition of immunoglobulin polypeptide chains, light (L) chains have two conformationally similar domains VL and CL; and heavy chains have four domains (VH, CH1, CH2, and CH3) each of which has one intrachain disulfide bridge.

25 30 Depending on the amino acid sequence of the constant (C)

domain of the heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM. The immunoglobulin class can be further divided into subclasses (isotypes), e.g., IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub>, IgG<sub>4</sub>, IgA<sub>1</sub>, and IgA<sub>2</sub>. The heavy-chain constant domains that correspond to the different classes of immunoglobulins are  $\alpha$ ,  $\delta$ ,  $\epsilon$ ,  $\gamma$ , and  $\mu$  domains respectively. The light chains of antibodies from any vertebrate species can be assigned to one of two distinct types called kappa ( $\kappa$ ) or lambda ( $\lambda$ ), based upon the amino acid sequence of their constant domains. Sequence studies have shown that the  $\mu$  chain of IgM contains five domains VH, CH $\mu$ 1, CH $\mu$ 2, CH $\mu$ 3, and CH $\mu$ 4. The heavy chain of IgE ( $\epsilon$ ) also contains five domains.

The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known. Of these IgA and IgM are polymeric and each subunit contains two light and two heavy chains. The heavy chain of IgG ( $\gamma$ ) contains a length of polypeptide chain lying between the CH $\gamma$ 1 and CH $\gamma$ 2 domains known as the hinge region. The  $\alpha$  chain of IgA has a hinge region containing an O-linked glycosylation site and the  $\mu$  and  $\epsilon$  chains do not have a sequence analogous to the hinge region of the  $\gamma$  and  $\alpha$  chains, however, they contain a fourth constant domain lacking in the others. The domain composition of immunoglobulin chains can be summarized as follows:

Light Chain  $\lambda = V\lambda C\lambda$   
 $\kappa = V\kappa C\kappa$

Heavy Chain IgG ( $\gamma$ ) = VH CH $\gamma$ 1, hinge CH $\gamma$ 2 CH $\gamma$ 3  
 IgM ( $\mu$ ) = VH CH $\mu$ 1 CH $\mu$ 2 CH $\mu$ 3 CH $\mu$ 4



IgA ( $\alpha$ ) = VH CH $\alpha$ 1 hinge CH $\alpha$ 2 CH $\alpha$ 3

IgE ( $\epsilon$ ) = VH CH $\epsilon$ 1 CH $\epsilon$ 2 CH $\epsilon$ 3 CH $\epsilon$ 4

IgD ( $\delta$ ) = VH CH $\delta$ 1 hinge CH $\delta$ 2 CH $\delta$ 3

5       The "CH2 domain" of a human IgG Fc region (also referred to  
as "Cy2" domain) usually extends from about amino acid 231 to  
about amino acid 340. The CH2 domain is unique in that it is not  
closely paired with another domain. Rather, two N-linked  
10       branched carbohydrate chains are interposed between the two CH2  
domains of an intact native IgG molecule.

      The "CH3 domain" comprises the stretch of residues C-  
terminal to a CH2 domain in an Fc region (*i.e.* from about amino  
acid residue 341 to about amino acid residue 447 of an IgG).

      "Hinge region" is generally defined as stretching from  
15       Glu216 to Pro230 of human IgG1 (Burton, *Molec. Immunol.*22:161-206  
(1985)). Hinge regions of other IgG isotypes may be aligned with  
the IgG1 sequence by placing the first and last cysteine residues  
forming inter-heavy chain S-S bonds in the same positions.

      The "lower hinge region" of an Fc region is normally defined  
20       as the stretch of residues immediately C-terminal to the hinge  
region, *i.e.* residues 233 to 239 of the Fc region.

      Papain digestion of antibodies produces two identical  
antigen-binding fragments, called "Fab" fragments or regions,  
each with a single antigen-binding site, and a residual "Fc"  
25       fragment or region (Figure 1). Although the boundaries of the Fc  
region of an immunoglobulin heavy chain might vary, the human IgG  
heavy chain Fc region is usually defined to stretch from an amino  
acid residue at position Cys226, or from Pro230, to the carboxyl-  
terminus thereof. The Fc region of an immunoglobulin generally  
30       comprises two constant domains, CH2 and CH3, as shown, for

example, in Fig. 1. A "native Fc region sequence" comprises an amino acid sequence identical to the amino acid sequence of an Fc region found in nature. Native human Fc region sequences are shown in Fig. 2 & 3 and include but are not limited to the human IgG1 Fc region (non-A and A allotypes); human IgG2 Fc region; human IgG3 Fc region; and human IgG4 Fc region as well as naturally occurring variants thereof. Native murine Fc regions sequences are shown in Fig. 2A.

Pepsin treatment yields an  $F(ab')_2$  fragment that has two antigen-combining sites and is still capable of cross-linking antigen. The Fab fragment contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxyl terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group.  $F(ab')_2$  antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

A "functional Fc region" possesses an "effector function" of a native Fc region. Exemplary "effector functions" include C1q binding; complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g. B cell receptor; BCR), etc. Such effector functions generally require the Fc region to be combined with a binding domain (e.g. a peptide ligand) and can be assessed using various assays known in the art.

By introducing the appropriate amino acid sequence

modifications in a parent or native Fc region, one can generate a variant Fc region which (a) mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of human effector cells more effectively and/or (b) binds an Fc gamma receptor (FcγR) with better affinity than the parent polypeptide. Such Fc region variants will generally comprise at least one amino acid modification in the Fc region. The variant Fc region may include two, three, four, five, etc substitutions therein.

Several antibody effector functions are mediated by Fc receptors (FcRs), which bind the Fc region of an antibody. FcRs are defined by their specificity for immunoglobulin isotypes; Fc receptors for IgG antibodies are referred to as FcγR, for IgE as FcεR, for IgA as FcαR and so on. Three subclasses of FcγR have been identified: FcγR I (CD64), FcγR II (CD32) and FcγR III (CD16). Because each FcγR subclass is encoded by two or three genes, and alternative RNA splicing leads to multiple transcripts, a broad diversity in FcγR isoforms exists. These different FcR subtypes are expressed on different cell types (reviewed in Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-492 (1991)). For example, in humans, FcγRIIIB is found only on neutrophils, whereas FcγRIIIA is found on macrophages, monocytes, natural killer (NK) cells, and a subpopulation of T-cells. Notably, FcγRIIIA is the only FcR present on NK cells, one of the cell types implicated in ADCC.

The binding site on human and murine antibodies for FcγR have been previously mapped to the lower hinge region (residues 233-239: EU index numbering as in Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)).

Woof *et al.* *Molec. Immunol.* 23:319-330 (1986); Duncan *et al.*

*Nature* 332:563 (1988); Canfield and Morrison, *J. Exp. Med.* 173:1483-1491 (1991); Chappel et al., *Proc. Natl. Acad. Sci USA* 88:9036-9040 (1991).

"Clq" is a polypeptide that includes a binding site for the Fc region of an immunoglobulin. Clq together with two serine proteases, Clr and C1s, forms the complex C1, the first component of the complement dependent cytotoxicity (CDC) pathway.

"Antibody-dependent cell-mediated cytotoxicity" and "ADCC" refer to a cell-mediated reaction in which nonspecific cytotoxic cells that express FcRs (e.g. Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and subsequently cause lysis of the target cell. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol* 9:457-92 (1991).

As used herein, the term "salvage receptor binding ligand" refers to an ligand of the Fc region of an IgG molecule (e.g., IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub>, or IgG<sub>4</sub>) that is responsible for increasing the *in vivo* serum half-life of the IgG molecule (U.S. Patent No. 5,739,277, issued April 14, 1998).

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those in which the disorder is to be prevented.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, horses, cats, cows, etc. Preferably, the mammal is human.

A "disorder" is any condition that would benefit from treatment with the compositions comprising the peptide ligands of the invention. This includes chronic and acute disorders or diseases including those pathological conditions which predispose the mammal to the disorder in question. Non-limiting examples of disorders to be treated herein include benign and malignant tumors; leukemias and lymphoid malignancies; neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders.

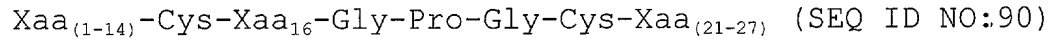
The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.

As used herein, the term "parenteral" refers to introduction of a compound of the invention into the body by other than the intestines, and in particular, intravenous (i.v.), intraarterial (i.a.), intraperitoneal (i.p.), intramuscular (i.m.), intraventricular, and subcutaneous (s.c.) routes.

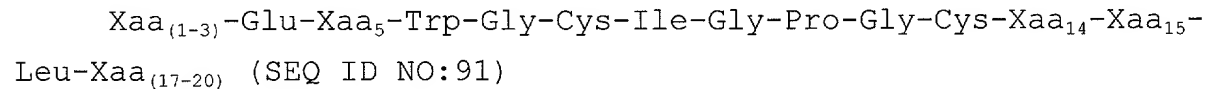
**Modes for Carrying out the Invention**

Peptide Ligands

Peptide ligands within the context of the present invention bind ErbB2 and can be identified by their ability to compete for binding ErbB2 in an in vitro assay with a peptide ligand having the general formula:



wherein  $\text{Xaa}_{(1-14)}$  is absent or between one and fourteen amino acids;  $\text{Xaa}_{16}$  is selected from the group consisting of Met, Thr, Cys and Ile and is preferably Ile;  $\text{Xaa}_{(21-27)}$  is absent or between one and 7 amino acids. Preferably the peptide ligand will compete for binding ErbB2 as described with a peptide ligand having the following general formula:



wherein  $\text{X}_{(1-3)}$  and  $\text{X}_{(17-20)}$  are, independently, absent or between one and three and one and four amino acids respectively and  $\text{Xaa}_1$ ,  $\text{Xaa}_2$  and  $\text{Xaa}_3$  are amino acids. In particular embodiments, the peptide ligand of the present invention will compete with any of the peptide ligands represented in SEQ ID NO: 1 - SEQ ID NO: 44 and SEQ ID NO: 57 - SEQ ID NO: 69 described herein and preferably will compete with SEQ ID NO: 14 for binding ErbB2.

As will be appreciated from the foregoing, the term "compete" and "ability to compete" are relative terms. Thus the terms, when used to describe the peptide ligands of the present invention, refer to peptide ligands that produce a 50% inhibition of binding of, for example, SEQ ID NO:14, when present at 50  $\mu\text{M}$ , preferably when present at 1  $\mu\text{M}$ , more preferably 100  $\mu\text{M}$ , and preferably when present at 1nM or less in a standard competition assay as described herein. Such peptide ligands will generally

bind ErbB2 with an affinity of less than about 1  $\mu$ M, preferably less about 100 nM and more preferably less than about 10 nM as determined by a standard competition assay such as the one described in the Example sections. However, peptide ligands having an affinity for ErbB2 of less than about 1 nM and preferably between about 1 pM and 1 nM are equally likely to be peptide ligands within the context of the present invention.

For in vitro assay systems to determine whether a compound has the ability to compete or competes with a peptide ligand described above, the skilled artisan can employ any of a number of standard competition assays. Such procedures include but are not limited to competitive assay systems using techniques such as radioimmunoassays, enzyme immunoassays (EIA), preferably the enzyme linked immunosorbent assay (ELISA), "sandwich" immunoassays, immunoradiometric assays, fluorescent immunoassays, and immunoelectrophoresis assays, to name but a few.

By way of exemplification and not limitation an ELISA assay can be conducted wherein microtiter plates (for example, Nunc Maxisorp™ 96-well plates, Inter Med, Denmark) are coated with HER2-ECD in 50 mM ammonium bicarbonate, pH 9.3, using 5  $\mu$ g/ml, overnight at 4°C. Wells can be blocked using PBS containing 1% BSA (PBS-BSA) for 1 hr at 25°C. Candidate peptide ligands are titrated in PBS-BSA and tested for their ability to block the binding of peptide 1.1.FI (SEQ ID NO: 14) produced as a Z protein fusion (1.1.FI-Z) as described herein and biotinylated (1.1.FI-Zb) to immobilized HER2-ECD. Following an incubation of about 1 hour the plate is washed with PBS-TWEEN and Streptavidin-HRP is added for about 30 min. Plates are washed again with PBS-TWEEN and the bound HRP assayed using ABTS/H<sub>2</sub>O<sub>2</sub> substrate. The change in absorbance at 405 nm is monitored. Decrease in absorbance is

plotted vs. sample concentration and an  $IC_{50}$  for each candidate peptide ligand is determined.

As previously noted, preferred peptide ligands of the present invention are non-naturally occurring peptide ligands of between about 10 and 30 amino acid residues and preferably about 20 amino acid residues. Especially preferred peptide ligands as described above consist of naturally occurring amino acids and can be generated using standard recombinant and synthetic techniques well known to the skilled artisan.

Preferred peptide ligands have the general formula:  
Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa. Somewhat more particularly, preferred peptide ligands have the formula:

$Xaa_{(1-7)}$ -Cys- $Xaa_9$ -Gly-Pro-Gly-Cys- $Xaa_{(14-20)}$  (SEQ ID NO:92)  
wherein  $X_{(1-7)}$  and  $Xaa_{(14-20)}$  are, independently, absent or between one and seven amino acids and  $Xaa_9$  is an amino acid selected from the group consisting of Met, Ile and Thr and is preferably Ile. Somewhat more particularly, preferred peptide ligands have the formula:

$Xaa_{(1-5)}$ -Trp- $Xaa_7$ -Cys- $Xaa_9$ -Gly-Pro-Gly-Cys- $Xaa_{(14-20)}$  (SEQ ID NO:93)

wherein  $Xaa_{(1-5)}$  is absent or between one and five amino acids and  $Xaa_7$  is selected from the group consisting of Asp, Gly, Glu and His and preferably Gly. More preferred according to this aspect of the invention, are peptide ligands having the following formula are preferred:

$Xaa_{(1-3)}$ -Glu- $Xaa_5$ -Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys- $Xaa_{14}$ - $Xaa_{15}$ -Leu- $Xaa_{(17-20)}$  (SEQ ID NO:91)

wherein  $Xaa_{(1-3)}$  is absent or between one and three amino acids,  $Xaa_5$  is an amino acid,  $Xaa_{13}$  is an amino acid,  $Xaa_{14}$  is an amino



acid and -Xaa<sub>(17-20)</sub> is absent or between one and four amino acids. Exemplary peptide ligands according to this aspect of the invention are peptide ligands wherein X<sub>(1-3)</sub>- is absent or selected from the group consisting of:

5 Gln-Arg-Asn-, Leu-Ser-Pro-, Glu-Asn-Trp-, Ala-Ser-His-, Lys-Leu-Asn-, Thr-Gln-Ala-, Ala-Pro-Arg-, Gln-Val-Tyr-, Arg-Thr-Glu-, Phe-Ala-Gly-, Thr-Ala-Arg-, Arg-Pro-His-, Asn-Val-Cys-, Cys-Ile-Asp-, Tyr-Glu-Trp-, Arg-Trp-Asp-, His-Trp-Met-, Asn-Trp-Pro-, Phe-Asn-Trp-, Phe-Ser-Gly-, Gly-Gly-Trp-, Leu-Trp-Phe-, Gly-Ile-Pro-, Trp-Trp-Thr-, Leu-Gly-Trp-, Ser-Pro-Trp-, Arg-Gly-Trp-, Tyr-Glu-Phe-, Tyr-Glu-Gly-, Tyr-Glu-Val-, Tyr-Ser-Phe-, Tyr-Asp-Phe-, Asp-Glu-Val-, Ser-Glu-Val-, Phe-Glu-Phe-, and His-Asp-Val-; Xaa<sub>5</sub> is selected from the group consisting of Ala, Thr, Met, Val, Arg, Glu, Asp, Ser, Gln, Pro, Gly, Phe and Lys; Xaa<sub>14</sub> is selected from the group consisting of Glu, Lys, Arg, Asp, Ser, Ala, Asn, Thr, Gly, Pro, Val and Gln, Xaa<sub>15</sub> is selected from the group consisting of Met, Phe, Ala, Cys, Gln, Glu, Trp, Leu, Val, Tyr, Thr, Ser and Asn, and -Xaa<sub>(17-20)</sub> is a four amino acid peptide having the following exemplary sequences:

20 -Phe-Gly-Ala-His (SEQ ID NO:94)  
 -Phe-Asp-Ala-His (SEQ ID NO:95)  
 -Leu-Glu-Ala-His (SEQ ID NO:96)  
 -Phe-Glu-Gly-His (SEQ ID NO:97)  
 -Phe-Gly-Ala-Leu (SEQ ID NO:98)  
 25 -Phe-Glu-Ala-Tyr (SEQ ID NO:99)  
 -Phe-Ala-Gly-His (SEQ ID NO:100) and  
 -Phe-Glu-Ala-Phe (SEQ ID NO:101).

Preferably -Xaa<sub>(17-20)</sub> is a four amino acid peptide having the following formula:

30 -Xaa<sub>17</sub>-Xaa<sub>18</sub>-Cys-Xaa<sub>20</sub>.

Exemplary peptide ligands according to this aspect of the invention are peptide ligands wherein -Xaa<sub>(17-20)</sub> is selected from the group consisting of:

-Gln-Ala-Cys-Met (SEQ ID NO:102)  
 5 -Leu-Gln-Cys-Trp (SEQ ID NO:103)  
 -Met-Ser-Cys-Val (SEQ ID NO:104)  
 -Leu-Arg-Cys-Ile (SEQ ID NO:105)  
 -Gln-Ala-Cys-Leu (SEQ ID NO:106)  
 -Leu-Ser-Cys-Leu (SEQ ID NO:107)  
 10 -Ile-Gly-Cys-Leu (SEQ ID NO:108)  
 -Leu-Ala-Cys-Leu (SEQ ID NO:109)  
 -Leu-Ser-Cys-Ile (SEQ ID NO:110)  
 -Met-Asn-Cys-Leu (SEQ ID NO:111)  
 -Leu-Arg-Cys-Leu (SEQ ID NO:112)  
 15 -Leu-Lys-Cys-Leu (SEQ ID NO:113)  
 -Leu-Gly-Cys-Leu (SEQ ID NO:114)  
 -Leu-Asn-Cys-Ile (SEQ ID NO:115)  
 -Met-Gly-Cys-Leu (SEQ ID NO:116) and  
 -Met-Ala-Cys-Leu (SEQ ID NO:117).

20 According to another embodiment of this aspect of the invention are peptide ligands wherein -Xaa<sub>(17-20)</sub> is a four amino acid peptide having the following formula:

-Cys-Xaa<sub>18</sub>-Xaa<sub>19</sub>-Cys

25 wherein Xaa<sub>18</sub> is an amino acid and Xaa<sub>19</sub> is an amino acid.

According to this aspect of the invention, exemplary peptide ligands comprise an -Xaa<sub>(17-20)</sub> selected from the group consisting of:

-Cys-Ala-Trp-Cys (SEQ ID NO:118)  
 30 -Cys-Ser-Trp-Cys (SEQ ID NO:119)

-Cys-Glu-Pro-Cys (SEQ ID NO:120)  
 -Cys-Asp-Trp-Cys (SEQ ID NO:121)  
 -Cys-Glu-Trp-Cys (SEQ ID NO:122)  
 -Cys-Asn-Trp-Cys (SEQ ID NO:123) and  
 5 -Cys-Gly-Trp-Cys (SEQ ID NO:124).

Exemplary peptide ligands according to this aspect of the invention include:

Gln-Arg-Asn-Glu-Ala-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Met-Leu-  
 Cys-Ala-Trp-Cys (SEQ ID NO:1)

10 Leu-Ser-Pro-Glu-Thr-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Met-Leu-  
 Cys-Ser-Trp-Cys (SEQ ID NO:2)

Glu-Asn-Trp-Glu-Met-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Lys-Phe-Leu  
 Cys-Glu-Pro-Cys (SEQ ID NO:3)

5 Glu-Val-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Lys-Ala-Leu-Cys-Asp-Trp-  
 Cys (SEQ ID NO:4)

Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Arg-Met-Leu-Cys-Glu-Trp-  
 Cys (SEQ ID NO:5)

Glu-Val-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Asp-Met-Leu-Cys-Asn-Trp-  
 Cys (SEQ ID NO:6)

10 Glu-Val-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ser-Met-Leu-Cys-Gly-Trp-  
 Cys (SEQ ID NO:7)

Xaa-Xaa-Xaa-Glu-Xaa-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Xaa-Met-Leu-  
 Cys-Xaa-Trp-Cys (SEQ ID NO:8)

Ala-Ser-His-Glu-Val-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Lys-Cys-Leu-  
 25 Gln-Ala-Cys-Met (SEQ ID NO:9)

Lys-Leu-Asn-Glu-Glu-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Cys-Leu  
 Leu-Gln-Cys-Trp (SEQ ID NO:10)

Lys-Leu-Asn-Glu-Asp-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Cys-Leu-  
 Leu-Xaa-Cys-Xaa (SEQ ID NO:11)

30 Thr-Gln-Ala-Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Cys-Leu-

Met-Ser-Cys-Val (SEQ ID NO:12)

Ala-Pro-Arg-Glu-Val-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Cys-Leu-  
Leu-Arg-Cys-Ile (SEQ ID NO:13)

Gln-Val-Tyr-Glu-Ser-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Cys-Leu-  
5 Gln-Ala-Cys-Leu (SEQ ID NO:14)

Arg-Thr-Glu-Glu-Gln-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Arg-Cys-Leu  
Leu-Ser-Cys-Leu (SEQ ID NO:15)

Phe-Ala-Gly-Glu-Ser-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Cys-Leu-  
Ile-Gly-Cys-Leu (SEQ ID NO:16)

10 Thr-Ala-Arg-Glu-Val-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Asn-Cys-Leu-  
Leu-Ala-Cys-Leu (SEQ ID NO:17)

Arg-Pro-His-Glu-Pro-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ser-Cys-Leu-  
Leu-Ser-Cys-Ile (SEQ ID NO:18)

Glu-Val-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Cys-Leu-Met-Asn-Cys-  
5 Leu (SEQ ID NO:19)

Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Cys-Leu-Leu-Arg-Cys-  
Leu (SEQ ID NO:20)

Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Gly-Cys-Leu-Leu-Lys-Cys-  
Leu (SEQ ID NO:21)

10 Glu-Pro-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Cys-Leu-Leu-Gly-Cys-  
Leu (SEQ ID NO:22)

Glu-Glu-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Cys-Leu-Leu-Asn-Cys-  
Ile (SEQ ID NO:23)

Glu-Gln-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Lys-Cys-Leu-Met-Gly-Cys-  
25 Leu (SEQ ID NO:24)

Glu-Gln-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Gly-Cys-Leu-Leu-Arg-Cys-  
Leu (SEQ ID NO:25)

Glu-Ala-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Gly-Cys-Leu-Met-Ala-Cys-  
Leu (SEQ ID NO:26)

30 Xaa-Xaa-Xaa-Glu-Xaa-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Xaa-Cys-Leu-

Leu-Xaa-Cys-Leu (SEQ ID NO:27)  
 Asn-Val-Cys-Glu-Phe-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Gln-Leu-  
 Cys (SEQ ID NO:28)  
 Cys-Ile-Asp-Glu-Thr-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Glu-Leu  
 5 Arg-Cys-Lys-Arg (SEQ ID NO:29)  
 Tyr-Glu-Trp-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Pro-Ala-Leu-  
 Gly-Phe-Gly-Tyr (SEQ ID NO:30)  
 Arg-Trp-Asp-Glu-Glu-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Trp-Leu-  
 Val-Val-Arg-Lys (SEQ ID NO:31)  
 10 His-Trp-Met-Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Gly-Phe-  
 Leu(SEQ ID NO:32)  
 Asn-Trp-Pro-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Lys-Leu-  
 Leu(SEQ ID NO:33)  
 Phe-Asn-Trp-Glu-Lys-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Arg-Thr-  
 15 Leu(SEQ ID NO:34)  
 Phe-Ser-Gly-Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Gln-Val-  
 Leu(SEQ ID NO:35)  
 Gly-Gly-Trp-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Arg-Tyr-  
 Leu(SEQ ID NO:36)  
 20 Leu-Trp-Phe-Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Thr-Xaa-  
 Leu(SEQ ID NO:37)  
 Gly-Ile-Pro-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Glu-Trp-  
 Leu(SEQ ID NO:38)  
 Trp-Trp-Thr-Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ser-Met-  
 25 Leu(SEQ ID NO:39)  
 Xaa-Cys-Xaa-Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ser-Met-  
 Leu(SEQ ID NO:40)  
 Leu-Gly-Trp-Glu-Arg-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Arg-Ala-  
 Leu(SEQ ID NO:41)  
 30 Ser-Pro-Trp-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Arg-Trp-

Leu (SEQ ID NO:42)

Arg-Gly-Trp-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ser-Phe-

Leu (SEQ ID NO:43)

Xaa-Xaa-Trp-Glu-Xaa-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Xaa-Xaa-Leu-

5 Xaa-Xaa-Xaa-Xaa (SEQ ID NO:44)

Tyr-Glu-Val-Glu-Ala-Trp-Asp-Cys-Met-Gly-Pro-Gly-Cys-Ala-Asn-Leu-

Phe-Glu-Ala-His (SEQ ID NO:57)

Tyr-Glu-Phe-Glu-Gly-Trp-Asp-Cys-Met-Gly-Pro-Gly-Cys-Ala-Ser-Val-

Phe-Gly-Ala-His (SEQ ID NO:58)

10 Tyr-Glu-Gly-Glu-Ser-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Ser-Leu-

Phe-Asp-Ala-His (SEQ ID NO:59)

Tyr-Glu-Val-Glu-Val-Trp-Glu-Cys-Ile-Gly-Pro-Gly-Cys-Gly-Tyr-Leu-

Phe-Gly-Ala-His (SEQ ID NO:60)

Tyr-Glu-Val-Glu-Gly-Trp-Gly-Cys-Met-Gly-Pro-Gly-Cys-Ala-Phe-Leu-

5 Leu-Glu-Ala-His (SEQ ID NO:61)

Tyr-Ser-Phe-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Tyr-Leu-

Phe-Glu-Gly-His (SEQ ID NO:62)

Tyr-Asp-Phe-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Gly-Asn-Leu-

Leu-Glu-Ala-His (SEQ ID NO:63)

20 Tyr-Asp-Phe-Glu-Gly-Trp-Asp-Cys-Thr-Gly-Pro-Gly-Cys-Ala-Tyr-Leu-

Phe-Glu-Gly-His (SEQ ID NO:64)

Asp-Glu-Val-Glu-Ser-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Tyr-Leu-

Phe-Gly-Ala-Leu (SEQ ID NO:65)

Ser-Glu-Val-Glu-Val-Trp-His-Cys-Ile-Gly-Pro-Gly-Cys-Val-Tyr-Leu-

25 Phe-Glu-Ala-Tyr (SEQ ID NO:66)

Phe-Glu-Phe-Glu-Gly-Trp-Glu-Cys-Met-Gly-Pro-Gly-Cys-Ala-Glu-Leu-

Phe-Ala-Gly-His (SEQ ID NO:67)

His-Asp-Val-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Asp-Leu-

Phe-Glu-Ala-Phe (SEQ ID NO:68)

30 Tyr-Glu-Phe-Glu-Gly-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Ala-Tyr-Leu-

Phe-Glu-Ala-His (SEQ ID NO:69)

including conservative amino acid substitutions within the foregoing exemplary amino acid sequences.

Further preferred peptide compounds also have the general formula:

Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys-Cys-Xaa-Xaa-Xaa-Cys-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-Cys (SEQ ID NO:125).

Somewhat more particularly the formula:

Xaa<sub>(1-10)</sub>-Glu-Xaa<sub>12</sub>-Trp-Xaa<sub>14</sub>-Cys-Cys-Gly-Pro-Gly-Cys-Xaa<sub>21</sub>-Xaa<sub>22</sub>-Xaa<sub>23</sub>-Xaa<sub>(24-27)</sub> (SEQ ID NO:126)

wherein Xaa<sub>(1-10)</sub> is absent or between 1 and 10 amino acids, Xaa<sub>12</sub> is an amino acid, Xaa<sub>14</sub> is an amino acid, Xaa<sub>21</sub> is an amino acid, Xaa<sub>22</sub> is an amino acid, Xaa<sub>23</sub> is an amino acid selected from the group consisting of Val and Leu and Xaa<sub>(24-27)</sub> is absent or between one and four amino acids. Preferably, according to this aspect of the invention, Xaa<sub>12</sub> is an amino acid selected from the group consisting of Val, Leu, Ser, Trp; Xaa<sub>14</sub> is an amino acid selected from the group consisting of Gln, Glu, Asp and His; Xaa<sub>21</sub> is an amino acid selected from the group consisting of Gly and Glu; Xaa<sub>22</sub> is an amino acid selected from the group consisting of Trp, Leu and Phe and Xaa<sub>23</sub> is Val.

Preferred peptide ligands according to this aspect of the invention include those wherein Xaa<sub>(1-10)</sub> is 10 amino acids having the following formula:

Cys-Xaa<sub>(2-7)</sub>-Cys-Xaa<sub>9</sub>-Gly- and wherein Xaa<sub>(24-27)</sub> is four amino acids having the following formula:

Xaa<sub>(24-26)</sub>-Cys and wherein Xaa<sub>(2-7)</sub> is six amino acids and Xaa<sub>(24-26)</sub> is 3 amino acids.

Preferred according to this aspect of the invention are peptide ligands wherein Xaa<sub>(1-10)</sub> has the following formula:

Cys-Xaa<sub>2</sub>-Trp-Val-Xaa<sub>5</sub>-Xaa<sub>6</sub>-Xaa<sub>7</sub>-Cys-Xaa<sub>9</sub>-Gly- (SEQ ID NO:127)

wherein

Xaa<sub>2</sub> is an amino acid selected from the group consisting of Ala and Ser, Xaa<sub>5</sub> is an amino acid selected from the group consisting of Ser, Leu, Ala, Arg and Val, Xaa<sub>6</sub> is an amino acid selected from the group consisting of Phe, Val and Leu, Xaa<sub>7</sub> is an amino acid selected from the group consisting of Asp, Gln, Tyr, Trp, Leu and His and Xaa<sub>9</sub> is an amino acid selected from the group consisting of Gly, Phe and Leu.

Preferred among this group of peptides are peptide ligands wherein Xaa<sub>(1-10)</sub> has the following formula:

Cys-Ala-Trp-Val-Leu-Xaa<sub>6</sub>-Xaa<sub>7</sub>-Cys-Gly-Gly- (SEQ ID NO:128) and

wherein Xaa<sub>(24-26)</sub> has the following formula:

Xaa<sub>24</sub>-Xaa<sub>25</sub>-Xaa<sub>26</sub> and Xaa<sub>24</sub> is an amino acid selected from the group consisting of Trp, Val, Gly and Ala, preferably Val; Xaa<sub>25</sub> is an amino acid selected from the group consisting of Asn, Lys, Asp, Glu and His, preferably Asn and Xaa<sub>26</sub> is an amino acid selected from the group consisting of Ala, Ser and Val and preferably Ala.

By way of exemplification and not limitation the following are suitable peptide ligands within the context of the present invention:

Cys-Ser-Trp-Val-Leu-Val-Gln-Cys-Gly-Gly-Glu-Trp-Trp-His-Cys-Cys-Gly-Leu-Gly-Cys-Gly-Leu-Val-Val-Asn-Ala-Cys (SEQ ID NO: 45)

Cys-Ala-Trp-Val-Ser-Phe-Glu-Cys-Gly-Gly-Glu-Val-Trp-His-Cys-Cys-Gly-Leu-Gly-Cys-Gly-Trp-Val-Trp-Lys-Ala-Cys (SEQ ID NO: 46)

Cys-Ala-Trp-Val-Leu-Val-Gln-Cys-Gly-Gly-Glu-Trp-Trp-His-Cys-Cys-Gly-Pro-Gly-Cys-Glu-Phe-Val-Val-Asp-Ala-Cys (SEQ ID NO: 47)

Cys-Ala-Trp-Val-Ala-Val-Tyr-Cys-Gly-Gly-Glu-Leu-Trp-His-Cys-Cys-Gly-Pro-Gly-Cys-Gly-Phe-Val-Val-Asp-Ser-Cys (SEQ ID NO: 48)

Cys-Ala-Trp-Val-Arg-Val-Trp-Cys-Phe-Gly-Glu-Trp-Trp-Asp-Cys-Cys-



Gly-Leu-Gly-Cys-Gly-Trp-Val-Val-Asn-Val-Cys (SEQ ID NO: 49)  
 Cys-Ala-Trp-Val-Arg-Val-Leu-Cys-Gly-Gly-Glu-Trp-Trp-His-Cys-Cys-  
 Gly-Leu-Gly-Cys-Gly-Trp-Val-Val-Glu-Ala-Cys (SEQ ID NO: 50)  
 Cys-Ser-Trp-Val-Ser-Val-Leu-Cys-Gly-Gly-Glu-Trp-Trp-Gln-Cys-Cys-  
 5 Gly-Pro-Gly-Cys-Gly-Leu-Val-Val-Asn-Ala-Cys (SEQ ID NO: 51)  
 Cys-Ser-Trp-Val-Ser-Leu-Gln-Cys-Gly-Gly-Glu-Trp-Trp-His-Cys-Cys-  
 Gly-Gly-Gly-Cys-Gly-Trp-Val-Val-Asn-Val-Cys (SEQ ID NO: 52)  
 Cys-Ser-Trp-Val-Leu-Leu-His-Cys-Gly-Gly-Glu-Trp-Trp-His-Cys-Cys-  
 Gly-Gly-Gly-Cys-Gly-Trp-Val-Gly-Glu-Ala-Cys (SEQ ID NO: 53)  
 10 Cys-Ser-Trp-Val-Leu-Leu-Glu-Cys-Gly-Gly-Glu-Leu-Trp-Glu-Cys-Cys  
 Gly-Leu-Gly-Cys-Gly-Trp-Val-Ala-Asp-Ala-Cys (SEQ ID NO: 54)  
 Cys-Ser-Trp-Val-Val-Phe-Glu-Cys-Leu-Gly-Glu-Ser-Trp-His-Cys-Cys-  
 Gly-Gly-Gly-Cys-Gly-Trp-Val-Val-His-Ala-Cys (SEQ ID NO: 55)  
 Cys-Ala-Trp-Val-Ser-Val-Glu-Cys-Gly-Gly-Glu-Trp-Trp-His-Cys-Cys-  
 15 Gly-Pro-Gly-Cys-Gly-Trp-Val-Val-Asp-Ala-Cys (SEQ ID NO: 56)

#### Peptide Ligand Combinations

##### A. Multimerization domains

According to a preferred embodiment of the invention, the  
 20 peptide ligands are combined with a multimerization domain.  
 According to this aspect of the invention, hybrid molecules are  
 provided which comprise at least two distinct domains. Each  
 molecule comprises a peptide ligand domain and a multimerization  
 domain. According to the present invention, the peptide ligand  
 25 domain is joined to a multimerization domain such as an  
 immunoglobulin Fc region, optionally via a flexible linker  
 domain.

The hybrid molecules of the present invention are  
 constructed by combining the peptide ligands with a suitable  
 30 multimerization domain. Ordinarily, when preparing the hybrid

molecules of the present invention, nucleic acid encoding the peptide ligand will be operably linked to nucleic acid encoding the multimerization domain sequence. Typically the construct encodes a fusion protein wherein the C-terminus of the peptide ligand is joined to the N-terminus or C-terminus, preferably the C-terminus of the multimerization domain. However, fusions where, for example, the N-terminus of the peptide ligand is joined to the N-terminus or C-terminus of the multimerization domain are also possible.

Preferred multimerization domains are immunoglobulin constant region sequences. Typically, in such fusions the encoded hybrid molecule will retain at least functionally active hinge, CH2 and CH3 domains of the constant region of an immunoglobulin heavy chain. Fusions are also made, for example, to the C-terminus of the Fc portion of a constant domain, or immediately N-terminal to the CH1 of the heavy chain or the corresponding region of the light chain.

The precise amino acid site at which the fusion of the peptide ligand to the immunoglobulin constant domain is made is not critical; particular sites are well known and may be selected in order to optimize the biological activity, secretion, or binding characteristics. In this regard, the skilled artisan may reference the construction of various immunoadhesins described in the literature (U.S. Patent No.s 5,116,964, 5,714,147 and 5,336,603; Capon et al., (1989) Nature 337:525-531; Traunecker et al., (1989) Nature 339:68-70; and Byrn et al., (1990) Nature 344:667-670; Watson et al., (1990) J. Cell. Biol. 110:2221-2229; Watson et al., (1991) Nature 349:164-167; Aruffo et al., (1990) Cell 61:1303-1313; Linsley et al., (1991) J. Exp. Med. 173:721-730; Lisley et al., J. Exp. Med. 174:561-569; Stamenkovic et al.,

Cell 66:1133-1144; Ashkenazi et al., (1991) Proc. Natl. Acad. Sci. USA 88:10535-10539; Lesslauer et al., (1991) Eur. J. Immunol. 27:2883-2886; and Peppel et al., (1991) J. Exp. Med. 174:1483-1489; Mohler et al., (1993) J. Immunol. 151:1548-1561);  
 5 Bennett et al., (1991) J. Biol. Chem. 266:23060-23067; Kurschner et al., (1992) J. Biol. Chem. 267:9354-9360; Chalupny et al., (1992) PNAS USA 89:10360-10364; Ridgway and Gorman, (1991) J. Cell. Biol. 115, Abstract No. 1448).

According to a particular aspect, an immunoglobulin type  
 10 multimerization domain is selected to provide a multimer such as a dimer having a functional Fc. In preferred aspects the multimerization domain is selected to provide an Fc domain having an effector function associated with a native immunoglobulin Fc region. Therefore, the peptide ligand is joined, in particular  
 15 aspects, to an immunoglobulin heavy chain constant domain to provide a multimer comprising a functional Fc domain selected for a particular effector function or functions. In this case, DNA encoding an immunoglobulin chain-peptide ligand sequence is typically coexpressed with the DNA encoding a second peptide  
 20 ligand-immunoglobulin heavy chain fusion protein. Upon secretion, the hybrid heavy chain will be covalently associated to provide an immunoglobulin-like structure comprising two disulfide-linked immunoglobulin heavy chains. The skilled artisan will recognize that effector functions include, for  
 25 example, C1q binding; complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; and down regulation of cell surface receptors (e.g. B cell receptor; BCR) and prolonging half-life through incorporation of the salvage receptor binding ligand as  
 30 described in, for example, U.S. patent no. 5,739,277 issued April

14, 1998.

Preferably, the Fc region is a human Fc region, e.g. a native sequence human Fc region human IgG1 (A and non-A allotypes), IgG2, IgG3 or IgG4 Fc region. Such sequences are shown in Figures 2 & 3. Additionally, by introducing the appropriate amino acid sequence modifications in a parent Fc region, one can generate a variant Fc region which (a) mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of human effector cells more effectively and/or (b) binds an Fc gamma receptor (Fc(R) with better affinity than the native sequence. Such Fc region variants will generally comprise at least one amino acid modification in the Fc region.

In a preferred embodiment, the peptide ligand sequence is fused to the N-terminus of the Fc region of immunoglobulin G<sub>1</sub> (IgG<sub>1</sub>). It is possible to fuse the entire heavy chain constant region to the peptide ligand sequence. However, more preferably, a sequence beginning in the hinge region just upstream of the papain cleavage site which defines IgG Fc chemically (*i.e.* residue 216, taking the first residue of heavy chain constant region to be 114), or analogous sites of other immunoglobulins is used in the fusion. In a particularly preferred embodiment, the peptide ligand amino acid sequence is fused to (a) the hinge region (or other linker domain) and CH2 and CH3 or (b) the CH1, hinge, CH2 and CH3 domains, of an IgG heavy chain. In a further preferred embodiment the peptide ligand amino acid sequence is fused to (a) the hinge region (or other linker domain) and (b) the CH3 domain of an IgG1 (see, for example, the constructs described in Hu et al., (1996) Cancer Res. 56:3055-3061).

According to a particular aspect of this embodiment, hybrid molecules comprising a peptide ligand and a multimerization

domain are assembled as multimers, for example homodimers, or heterodimers or even heterotetramers. Homodimers result from the pairing or crosslinking of two monomers comprising a peptide ligand and a multimerization domain. However, it is not essential that two identical monomers pair. According to a particular aspect of the invention a hybrid molecule as defined herein comprising a peptide ligand and a multimerization domain such as an immunoglobulin constant domain may pair with a companion immunoglobulin chain comprising one arm of an immunoglobulin. Various exemplary assembled hybrid molecules within the scope of the present invention are schematically diagramed below:

- (a) ACH
- (b) ACH-ACH
- (c) ACH-VHCH-VLCL
- (d) ACH-VHCH

wherein each A represents identical or different peptide ligands; VL is an immunoglobulin light chain variable domain; VH is an immunoglobulin heavy chain variable domain; CL is an immunoglobulin light chain constant domain and CH is an immunoglobulin heavy chain constant domain.

In the interests of brevity, the foregoing structures only show key features; they do not show optional linker domains between the peptide ligand domains and the multimerization domains as described herein below; they do not indicate joining, hinge or other domains of the immunoglobulins, nor are disulfide bonds shown. However, where such domains are required for binding activity, they are constructed to be present in the

ordinary locations which they occupy in the immunoglobulin molecules.

Although the presence of an immunoglobulin light chain is not required in the hybrid molecules of the present invention, an immunoglobulin light chain might be present either covalently associated to a peptide ligand-immunoglobulin heavy chain fusion polypeptide, or directly fused to the peptide ligand. In the former case, DNA encoding an immunoglobulin light chain is typically coexpressed with the DNA encoding the peptide ligand-immunoglobulin heavy chain fusion protein. Upon secretion, the hybrid heavy chain and the light chain will be covalently associated to provide an immunoglobulin-like structure comprising two disulfide-linked immunoglobulin heavy chain-light chain pairs.

The hybrid molecules described herein are most conveniently constructed by fusing the cDNA sequence encoding the peptide ligand portion in-frame to an immunoglobulin cDNA sequence. However, fusion to genomic immunoglobulin fragments can also be used (see, e.g. Aruffo et al., (1990), Cell 61:1303-1313; and Stamenkovic et al. (1991), Cell 66:1133-1144). The latter type of fusion requires the presence of Ig regulatory sequences for expression. cDNAs encoding IgG heavy-chain constant regions can be isolated based on published sequences from cDNA libraries derived from spleen or peripheral blood lymphocytes, by hybridization or by polymerase chain reaction (PCR) techniques. The cDNAs encoding the peptide ligand and the immunoglobulin parts of the hybrid molecule are inserted in tandem into a plasmid vector that directs efficient expression in the chosen host cells.

Alternatively, and especially in embodiments where the

peptide ligand is synthesized by, for example standard solid phase synthesis techniques, the peptide ligand may be linked to the multimerization domain by any of a variety of means familiar to those of skill in the art. Covalent attachment is typically the most convenient, but other forms of attachment may be employed depending upon the application. Examples of suitable forms of covalent attachment include the bonds resulting from the reaction of molecules bearing activated chemical groups with amino acid side chains in the multimerization domain and can be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutarealdehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene).

The invention includes the specific targeting of, for example HER2 bearing cell types, in vivo via the peptide ligands and according to this aspect of the present invention, conferring an Fc effector function such as Fc receptor binding, complement fixation, protein A binding, increasing half-life or crossing the blood brain barrier to the molecule.

#### B. Peptide Ligand Fusions

According to the present invention, the peptide ligand domain is optionally linked to, for example, another peptide ligand domain either directly or via a flexible peptide linker as

described below. According to the present invention, the linker domain, is any group of molecules that provides a spatial bridge between two or more peptide ligand domains as described in more detail herein below. According to this aspect of the invention, peptide ligands are linked together, as for example in a fusion protein. The hybrid molecules of this aspect of the invention are useful in, for example, cross-linking two or more receptors.

### C. Linker Domains

According to the present invention, the peptide ligand domain is optionally linked to, for example, another peptide ligand domain or a multimerization domain via a flexible peptide linker. The linker component of the hybrid molecule of the invention does not necessarily participate in but may contribute to the function of the hybrid molecule. Therefore, according to the present invention, the linker domain, is any group of molecules that provides a spatial bridge between two or more peptide ligand domains or a peptide ligand domain and a multimerization domain.

The linker domain can be of variable length and makeup. It is generally, the orientation caused by the linker domain and not its chemical structure that is important. The linker domain preferably allows for the peptide ligand domain of the hybrid molecule to bind, substantially free of spacial/conformational restrictions to the coordinant ErbB2 molecule. Therefore, the length of the linker domain is dependent upon the character of the two functional, e.g., the peptide ligand and the multimerization domains of the hybrid molecule.

One skilled in the art will recognize that various combinations of atoms provide for variable length molecules based



upon known distances between various bonds (Morrison, and Boyd, Organic Chemistry, 3rd Ed, Allyn and Bacon, Inc., Boston, MA (1977)). For example, the linker domain may be a polypeptide of variable length. The amino acid composition of the polypeptide determines the character and length of the linker. Exemplary, linker domains comprises between 2 and 10 amino acids, preferably about 6 amino acids as, for example, Gly-Gly-Gly-Ser-Gly-Gly (SEQ ID NO:129), Gly-Gly-Gly-Ser-Ser-Gly (SEQ ID NO:130), and Gly-Gly-Gly-Arg-Gly-Gly (SEQ ID NO:131).

#### D. Other Bispecific Combinations

According to certain aspects of the invention, bi- or dual-specific compositions comprising at least one peptide ligand domain are envisioned. For example, bispecific antibody compositions have been produced using leucine zippers (Kostelny et al., (1992) J. Immunol., 148(5):1547-1553). The leucine zipper peptides from the Fos and Jun proteins are linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers can be reduced at the hinge region to form monomers and then re-oxidized to form antibody heterodimers. This method can also be utilized for the production of peptide ligand homodimer and heterodimers utilizing the peptide ligands in place of the binding domains of the antibody heterodimers.

#### Recombinant Synthesis

The present invention encompasses a composition of matter comprising isolated nucleic acid, preferably DNA, encoding a peptide described herein. DNAs encoding the peptides of the invention can be prepared by a variety of methods known in the art. These methods include, but are not limited to, chemical

synthesis by any of the methods described in Engels et al.,  
 (1989) Agnew. Chem. Int. Ed. Engl., 28:716-734, the entire  
 disclosure of which is incorporated herein by reference, such as  
 the triester, phosphite, phosphoramidite and H-phosphonate  
 5 methods. In one embodiment, codons preferred by the expression  
 host cell are used in the design of the encoding DNA.  
 Alternatively, DNA encoding the peptide can be altered to encode  
 one or more variants by using recombinant DNA techniques, such as  
 site specific mutagenesis (Kunkel et al., (1991) Methods Enzymol.  
 10 204:125-139; Carter, P., et al., (186) Nucl. Acids. Res. 13:4331;  
 Zoller, M. J. et al., (1982) Nucl. Acids Res. 10:6487), cassette  
 mutagenesis (Wells, J. A., et al., (1985) Gene 34:315),  
 restriction selection mutagenesis (Wells, J. A., et al., (1986)  
 Philos. Trans, R. Soc. London SerA 317, 415), and the like.

The invention further comprises an expression control  
 sequence operably linked to the DNA molecule encoding a peptide  
 of the invention, and an expression vector, such as a plasmid,  
 comprising the DNA molecule, wherein the control sequence is  
 recognized by a host cell transformed with the vector. In  
 20 general, plasmid vectors contain replication and control  
 sequences which are derived from species compatible with the host  
 cell. The vector ordinarily carries a replication site, as well  
 as sequences which encode proteins that are capable of providing  
 phenotypic selection in transformed cells.

25 Suitable host cells for expressing the DNA include  
 prokaryote, yeast, or higher eukaryote cells. Suitable  
 prokaryotes include but are not limited to eubacteria, such as  
 Gram-negative or Gram-positive organisms, for example,  
 Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are  
 30 publicly available, such as *E. coli* K12 strain MM294 (ATCC

31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635).

In addition to prokaryotes, eukaryotic organisms, such as yeasts, or cells derived from multicellular organisms can be used as host cells. For expression in yeast host cells, such as common baker's yeast or *Saccharomyces cerevisiae*, suitable vectors include episomally replicating vectors based on the 2-micron plasmid, integration vectors, and yeast artificial chromosome (YAC) vectors. Suitable host cells for expression also are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. For expression in insect host cells, such as Sf9 cells, suitable vectors include baculoviral vectors. For expression in plant host cells, particularly dicotyledonous plant hosts, such as tobacco, suitable expression vectors include vectors derived from the Ti plasmid of *Agrobacterium tumefaciens*.

Examples of useful mammalian host cells include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., (1977) J. Gen Virol., 36:59); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, (1980) Proc. Natl. Acad. Sci. USA, 77:4216); mouse sertoli cells (TM4, Mather, (1980) Biol. Reprod., 23:243-251); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562,

ATCC CCL51); TRI cells (Mather et al., (1982) Annals N.Y. Acad. Sci., 383:44-68); MRC 5 cells; FS4 cells; and a human hepatoma cell line (Hep G2).

For expression in prokaryotic hosts, suitable vectors include pBR322 (ATCC No. 37,017), phGH107 (ATCC No. 40,011), pBO475, pS0132, pRIT5, any vector in the pRIT20 or pRIT30 series (Nilsson and Abrahmsen, (1990) Meth. Enzymol., 185:144-161), pRIT2T, pKK233-2, pDR540 and pPL-lambda. Prokaryotic host cells containing the expression vectors of the present invention include *E. coli* K12 strain 294 (ATCC NO. 31446), *E. coli* strain JM101 (Messing et al., (1981) Nucl. Acid Res., 9:309), *E. coli* strain B, *E. coli* strain  $\chi$ 1776 (ATCC No. 31537), *E. coli* c600 (Appleyard, *Genetics*, 39: 440 (1954)), *E. coli* W3110 (F-, gamma-, prototrophic, ATCC No. 27325), *E. coli* strain 27C7 (W3110, *tonA*, *phoA* *E15*, (*argF-lac*)169, *ptr3*, *degP41*, *ompT*, *kan<sup>r</sup>*) (U.S. Patent No. 5,288,931, ATCC No. 55,244), *Bacillus subtilis*, *Salmonella typhimurium*, *Serratia marcesans*, and *Pseudomonas* species.

For expression in mammalian host cells, useful vectors include vectors derived from SV40, vectors derived from cytomegalovirus such as the pRK vectors, including pRK5 and pRK7 (Suva et al., (1987) *Science*, 237:893-896; EP 307,247 (3/15/89), EP 278,776 (8/17/88)) vectors derived from vaccinia viruses or other pox viruses, and retroviral vectors such as vectors derived from Moloney's murine leukemia virus (MoMLV).

Optionally, the DNA encoding the peptide of interest is operably linked to a secretory leader sequence resulting in secretion of the expression product by the host cell into the culture medium. Examples of secretory leader sequences include stII, ecotin, lamB, herpes GD, lpp, alkaline phosphatase, invertase, and alpha factor. Also suitable for use herein is the

36 amino acid leader sequence of protein A (Abrahmsen et al., (1985) EMBO J., 4:3901).

Host cells are transfected and preferably transformed with the above-described expression or cloning vectors of this invention and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

Transfection refers to the taking up of an expression vector by a host cell whether or not any coding sequences are in fact expressed. Numerous methods of transfection are known to the ordinarily skilled artisan, for example,  $\text{CaPO}_4$  precipitation and electroporation. Successful transfection is generally recognized when any indication of the operation of this vector occurs within the host cell.

Transformation means introducing DNA into an organism so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in section 1.82 of Sambrook et al., Molecular Cloning (2nd ed.), Cold Spring Harbor Laboratory, NY (1989), is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., (1983) Gene, 23:315 and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method described in sections 16.30-16.37 of Sambrook et al., supra, is preferred. General aspects of mammalian cell host system transformations have been described by Axel in U.S. 4,399,216 issued 16 August 1983.

Transformations into yeast are typically carried out according to the method of Van Solingen et al., (1977) J. Bact., 130:946 and Hsiao et al., (1979) Proc. Natl. Acad. Sci. (USA), 76:3829. However, other methods for introducing DNA into cells such as by nuclear injection, electroporation, or by protoplast fusion may also be used.

Other preferred vectors can be constructed using standard techniques by combining the relevant traits of the vectors described above. Relevant traits include the promoter, the ribosome binding site, the gene of interest or gene fusion (the Z domain of protein A and the gene of interest and a linker), the antibiotic resistance markers, and the appropriate origins of replication. A variation on the above procedures contemplates the use of gene fusions, wherein the gene encoding the desired peptide is associated, in the vector, with a gene encoding another protein or a fragment of another protein. This results in the desired peptide being produced by the host cell as a fusion with another protein or peptide. The "other" protein or peptide is often a protein or peptide which can be secreted by the cell, making it possible to isolate and purify the desired peptide from the culture medium and eliminating the necessity of destroying the host cells which arises when the desired peptide remains inside the cell. Alternatively, the fusion protein can be expressed intracellularly. It is useful to use fusion proteins that are highly expressed.

The use of gene fusions, though not essential, can facilitate the expression of heterologous peptides in insect cells as well as the subsequent purification of those gene products. Protein A fusions are often used because the binding of protein A, or more specifically the Z domain of protein A, to

IgG provides an "affinity handle" for the purification of the fused protein. For example, a DNA sequence encoding the desired peptide ligand can be fused by site directed mutagenesis to the gene for a consensus domain of protein A known as the Z domain (Nilsson et al., (1987) Protein Engineering 1:107-113). After expression and secretion the fusion protein can be enzymatically cleaved to yield free peptide which can be purified from the enzymatic mix (see, e.g., Varadarajan et al., (1985) Proc. Natl. Acad. Sci USA 82:5681-5684; Castellanos-Serra et al., (1996) FEBS Letters 378:171-176; Nilsson et al., (1996) J. Biotechnol. 48:241-250).

Fusion proteins can be cleaved using chemicals, such as cyanogen bromide, which cleaves at a methionine, or hydroxylamine, which cleaves between an Asn and Gly residue. Using standard recombinant DNA methodology, the nucleotide base pairs encoding these amino acids may be inserted just prior to the 5' end of the gene encoding the desired peptide.

Alternatively, one can employ proteolytic cleavage of fusion protein. Carter, in Protein Purification: From Molecular Mechanisms to Large-Scale Processes, Ladisch et al., eds. (American Chemical Society Symposium Series No. 427, 1990), Ch 13, pages 181-193.

Proteases such as Factor Xa, thrombin, and subtilisin or its mutants, and a number of others have been successfully used to cleave fusion proteins. Preferred according to the present invention for the production of peptide ligands of less than about 30 amino acids is the protease trypsin which is highly specific for Arg and Lys residues. Trypsin cleavage is discussed generally in Nilsson et al. (1996) J. Biotech. 48:241 and Smith et al., Methods Mol. Biol. 32:289. Typically, a peptide linker

that is amenable to cleavage by the protease used is inserted between the "other" protein (e.g., the Z domain of protein A) and the desired peptide. Using recombinant DNA methodology, the nucleotide base pairs encoding the linker are inserted between the genes or gene fragments coding for the other proteins. Proteolytic cleavage of the partially purified fusion protein containing the correct linker can then be carried out on either the native fusion protein, or the reduced or denatured fusion protein.

The peptide may or may not be properly folded when expressed as a fusion protein. Also, the specific peptide linker containing the cleavage site may or may not be accessible to the protease. These factors determine whether the fusion protein must be denatured and refolded, and if so, whether these procedures are employed before or after cleavage.

When denaturing and refolding are needed, typically the peptide is treated with a chaotrope, such as guanidine HCl, and is then treated with a redox buffer, containing, for example, reduced and oxidized dithiothreitol or glutathione at the appropriate ratios, pH, and temperature, such that the peptide is refolded to its native structure.

The host cells referred to in this disclosure encompass cells in in vitro culture as well as cells that are within a host animal.

In cyclized embodiments of the invention, the recombinantly produced peptide can be cyclized by formation of an intramolecular disulfide bond as described above.

#### Utility

Generally speaking, the peptide ligands and hybrid molecules



of the present invention can be used in the same applications as, for example, native or variant heregulin molecules or antibodies directed against ErbB2 may be used. Of course, some peptide ligands or hybrid molecules within the scope of the present invention may be better suited for a particular application than another application. Those skilled in the art will readily ascertain which molecules are appropriate for a given application by using one or more conventional biological assay to determine the biological activity of the peptide ligand or hybrid molecule.

As but an example, heregulins are useful in the treatment of a variety of disorders, for example, disorders and diseases affecting the nervous system, musculature and epithelia. For example, an agonist peptide ligand or hybrid molecule of the present invention may be used in promoting the development, maintenance and or regeneration of a neuron in vivo in the same manner that heregulin or a heregulin variant may be used.

Diseases or disorders amenable to treatment with peptide ligands or hybrid molecules according to this aspect of the invention include, for example, central nervous system damage attendant to trauma, surgery, stroke, ischemia, infection, metabolic disorders nutritional deficiency, malignancy or a toxic agent.

Neurodegenerative disorders may also be treated included but not limited to human neurodegenerative diseases or disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Downs syndrome, nerve deafness and Meniere's disease. As well, particular peptide ligands are suited for use in the treatment of neuropathy, such as peripheral neuropathy associated with systemic diseases or disorders such as diabetes.

Agonist peptide ligands which upon binding ErbB2 initiate a

phosphorylation event as described are especially useful the foregoing aspects of the invention. Specific agonist peptide ligands of the invention are capable of enhancing the survival of cells, which is to say they increase the period of survival of an ErbB2 bearing cell either in vivo or in vitro relative to the period of survival of cells that have not been exposed to a particular agonist peptide ligand. In preferred embodiments, the agonist peptide ligand causes or enhances the proliferation of ErbB2 bearing cell types, either in vivo or in vitro, as quantified by, for example, measuring <sup>3</sup>H-thymidine uptake by cells. Proliferation may be associated with differentiation of ErbB2 cells as determined by screening an ErbB2 bearing cell population for phenotypic changes.

According to another aspect of the present invention, certain peptide ligands and hybrid molecules, especially those that bind ErbB2 but do not elicit an agonist associated response, are useful in, for example, inhibiting tumor cell invasion and metastasis as described more fully herein below. For example, a tumor that expresses ErbB2 receptors (especially one which overexpresses ErbB2) can be treated using a peptide ligand or hybrid molecule conjugated to a cytotoxic agent or in targeting a prodrug to cells expressing ErbB2.

#### A. Effector Function Engineering

For example, it may be desirable to modify the multimerization domain of hybrid molecules of the present invention with respect to effector function, to, for example, enhance the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced in an immunoglobulin Fc region, thereby allowing interchain disulfide

bond formation in this region. The homo- or heterodimeric hybrid molecule thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., (1992) J. Exp Med. 176:1191-1195 and Shopes, B. (1992) J. Immunol. 148:2918-2922. Homodimeric hybrid molecules with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al. (1993) Cancer Research 53:2560-2565.

Alternatively, an heterodimeric hybrid molecule can be engineered which has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al. (1989) Anti-Cancer Drug Design 3:219-230.

#### B. Conjugates

The invention also pertains to conjugates comprising the peptide ligands or any of the hybrid molecules described herein conjugated to a cytotoxic agent such as a chemotherapeutic agent, such as a protein toxin or cytotoxic drug or toxin (e.g. an enzymatically active toxin of bacterial, fungal, plant or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described. A chemotherapeutic agent is a chemical compound useful in the treatment of cancer including carcinoma, lymphoma, blastoma, sarcoma, and leukemias. Examples of chemotherapeutic agents include, antibiotics isolated from microorganisms such as the calicheamicins (Lee et al., (1987) J. Am. Chem. Soc. 109:3464-3466; Hinman et al., (1993) Cancer Res. 53:3336-3342), maytansinoids (such as those described

in Liu et al. (1996) Proc. Natl. Acad. Sci. USA 93:8618-8323),  
 Adriamycin, Doxorubicin, 5-Fluorouracil, Cytosine arabinoside,  
 Cyclophosphamide, thiotepa, Busulfan, Cytosin, Taxol,  
 Methotrexate, Cisplatin, Melphalan, Vinblastin, Bleomycin,  
 5 Etoposide, Ifosfamide, Mitomycin C, Mitosantrone, Vincristine,  
 Vinorelbine, Carboplatin, Teniposide, Daunomycin, Carminomycin,  
 Aminopterin, Dactinomycin, a Mitomycin, Nicotinamide, an  
 Espeeramicin, Melphalan and any related nitrogen mustard, and  
 endocrine therapeutics (such as diethylstilbestrol, Tamoxifen,  
 10 LHRH-antagonizing drugs, a progestin, an anti-progestin, etc.)

Enzymatically active toxins and fragments thereof which can  
 be used include diphtheria A chain, nonbinding active fragments  
 of diphtheria toxin, exotoxin A chain (from *Pseudomonas*  
*aeruginosa*), ricin A chain, abrin A chain, modeccin A chain,  
 5 alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins,  
*Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica  
 charantia inhibitor, curcin, croton, sapaonaria officinalis  
 inhibitor, gelonin, mitogellin, restrictocin, phenomycin,  
 enomycin and the tricothecenes.

A variety of radionuclides are available for the production  
 of radioconjugated peptide ligands or hybrid molecules. Examples  
 include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$  and  $^{186}\text{Re}$ . Carbon-14-labeled 1-  
 isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid  
 (MX-DTPA) is an exemplary chelating agent for conjugation of  
 25 radionucleotide to the hybrid molecules.

Conjugates of the peptide ligand or hybrid molecule and a  
 cytotoxic agent are made using a variety of bifunctional protein  
 coupling agents such as N-succinimidyl-3-(2-pyridyldithiol)  
 propionate (SPDP), iminothiolane (IT), bifunctional derivatives  
 30 of imidoesters (such as dimethyl adipimidate HCL), active esters

(such as disuccinimidyl suberate), aldehydes (such as glutaredehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared essentially as described in Vitetta et al. (1987) Science 238: 1098.

In another embodiment, the peptide ligand or hybrid molecules may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the peptide ligand or hybrid molecule-receptor conjugate is administered to a patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g. avidin) which is conjugated to a cytotoxic agent (e.g. a radionucleotide).

### C. Liposomes

The hybrid molecules or peptide ligands disclosed herein may also be formulated as liposomes. Liposomes containing the hybrid molecules are prepared by methods known in the art, such as described in Epstein et al., (1985) Proc. Natl. Acad. Sci. USA, 82:3688; Hwang et al., (1980) Proc. Natl Acad. Sci. USA, 77:4030; and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded

through filters of defined pore size to yield liposomes with the desired diameter. For example, hybrid molecules comprising an immunoglobulin constant domain as described herein can be conjugated to the liposomes as described in Martin et al. *J. Biol. Chem.* 257: 286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon et al. *J. National Cancer Inst.* 81(19)1484 (1989).

#### D. Enzyme Mediated Prodrug Therapy

The peptide ligands or hybrid molecules of the present invention may also be used in the manner of antibodies of antibody dependent enzyme mediated prodrug therapy (ADEPT) by conjugating the peptide ligand or hybrid molecules to a prodrug-activating enzyme which converts a prodrug (e.g. a peptidyl chemotherapeutic agent, see WO81/01145) to an active anti-cancer drug. See, for example, WO 88/07378 and U.S. Patent No. 4,975,278.

The enzyme component of the conjugate useful for ADEPT-type therapy includes any enzyme capable of acting on a prodrug in such a way so as to covert it into its more active, cytotoxic form. Enzymes that are useful in the method of this invention include, but are not limited to, alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic 5-fluorocytosine into the anti-cancer drug, 5-fluorouracil; proteases, such as serratia protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into

free drugs; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as  $\beta$ -galactosidase and neuraminidase useful for converting glycosylated prodrugs into free drugs;  $\beta$ -lactamase  
5 useful for converting drugs derivatized with  $\beta$ -lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Alternatively, antibodies with  
10 enzymatic activity, also known in the art as "abzymes", can be used to convert the prodrugs of the invention into free active drugs (see, e.g., Massey, (1987) Nature 328:457-458). Peptide ligand/hybrid molecule-abzyme conjugates can be prepared as described herein for delivery of the abzyme to a tumor cell  
15 population.

Enzymes can be covalently bound to the hybrid molecules by techniques well known in the art such as the use of the heterobifunctional crosslinking reagents discussed above. Alternatively, fusion proteins comprising at least the peptide  
20 ligand portion of the hybrid molecule of the invention linked to at least a functionally active portion of an enzyme of the invention can be constructed using recombinant DNA techniques well known in the art (see, e.g., Neuberger et al., (1984) Nature, 312:604-608).

#### 25 E. Pharmaceutical Compositions

Pharmaceutical compositions which comprise the peptide ligands of the invention may be administered in any suitable manner, including parental, topical, oral, or local (such as  
30 aerosol or transdermal) or any combination thereof. Suitable

regimens also include an initial administration by intravenous bolus injection followed by repeated doses at one or more intervals.

Pharmaceutical compositions of the compounds of the invention are prepared for storage by mixing a peptide ligand containing compound having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

The compositions herein may also contain more than one



active compounds as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, it may be desirable to further provide molecules, such as antibodies which bind to EGFR, ErbB2 (e.g. an antibody which binds a different ligand on ErbB2), ErbB3, ErbB4, or vascular endothelial factor (VEGF) in the one formulation. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine, growth inhibitory agent and/or cardioprotectant. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

#### F. Diagnosing and Prognosing a Disorder

Disorders for prognosis and diagnosis within the context of the present invention are preferably a benign or malignant tumor characterized by the overexpression of the ErbB2 receptor, e.g. a cancer, such as, breast cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer. Therefore, one embodiment of the present invention is directed to the detection and/or measurement of Erb2 in a sample and the use of such detection or measurement in the diagnosis, staging, determination of severity, and prognosis in general of the disorder.

In a particular embodiment, the diagnostic techniques described can be used to follow the progress of therapy. In a

subject undergoing therapeutic treatment that results in an increase or a decrease in the amount of Erb2 bearing cells, the amount of Erb2 bearing cells in a sample may serve as a useful measure for the success or failure of the treatment. Thus, the present invention provides a method for monitoring the effect of a therapeutic treatment in a subject which comprises measuring at suitable time intervals the amount of Erb2 expressed in a sample of tissue suspected of containing Erb-2 expressing cells. The total amount of Erb2 is compared to a "baseline" or "control" value which depending on the disease, and the treatment, may be the amount of Erb2 in a similar sample from a normal subject, from the patient prior to disease onset or during remission of disease, or from the patient prior to the initiation of therapy. One of ordinary skill in the art will readily discern the appropriate baseline value to use in a particular situation without undue experimentation.

Any procedure known in the art for the measurement of analytes can be used in the practice of the measurement of Erb2 in a sample using the compounds of the present invention. Such procedures include but are not limited to competitive and non-competitive assay systems using techniques such as radioimmunoassays, enzyme immunoassays (EIA), preferably the enzyme linked immunosorbent assay (ELISA), "sandwich" immunoassays, precipitin reactions, gel diffusion reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, and immunoelectrophoresis assays, to name but a few. For examples of preferred immunoassay methods, see U.S. Patents No. 4,845,026 (July 4, 1989) and No. 5,006,459 (April 9, 1991).

For diagnostic and prognostic applications, a compound of the present invention, typically a hybrid molecule as described herein above will be labeled with a detectable moiety and used to detect Erb-2 in a sample as described above. Numerous labels are available which can be preferably grouped into the following categories:

(a) Radioisotopes, such as  $^{35}\text{S}$ ,  $^{14}\text{C}$ ,  $^{125}\text{I}$ ,  $^3\text{H}$ , and  $^{131}\text{I}$ . The hybrid molecules can be labeled with the radioisotope using the techniques described in *Current Protocols in Immunology*, Volumes 1 and 2, Coligen et al., Ed., Wiley-Interscience, New York, New York, Pubs., (1991) for example and radioactivity can be measured using scintillation counting.

(b) Fluorescent labels such as rare earth chelates (europium chelates) or fluorescein and its derivatives, rhodamine and its derivatives, dansyl, Lissamine, phycoerythrin and Texas Red are available. The fluorescent labels can be conjugated to the hybrid molecules using the techniques disclosed in *Current Protocols in Immunology, supra*, for example. Fluorescence can be quantified using a fluorimeter.

(c) Various enzyme-substrate labels are available and U.S. Patent No. 4,275,149 provides a review of some of these. The enzyme preferably catalyses a chemical alteration of the chromogenic substrate which can be measured using various techniques. For example, the enzyme may catalyze a color change in a substrate, which can be measured spectrophotometrically. Alternatively, the enzyme may alter the fluorescence or chemiluminescence of the substrate. Techniques for quantifying a change in fluorescence are described above. The chemiluminescent substrate becomes electronically excited by a chemical reaction and may then emit light which can be measured (using a

chemiluminometer, for example) or donates energy to a fluorescent acceptor. Examples of enzymatic labels include luciferases (e.g., firefly luciferase and bacterial luciferase; U.S. Patent No. 4,737,456), luciferin, 2,3-dihydrophthalazinediones, malate dehydrogenase, urease, peroxidase such as horseradish peroxidase (HRPO), alkaline phosphatase,  $\beta$ -galactosidase, glucoamylase, lysozyme, saccharide oxidases (e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase), heterocyclic oxidases (such as uricase and xanthine oxidase), lactoperoxidase, microperoxidase, and the like. Techniques for conjugating enzymes to antibodies are described in O'Sullivan et al., Methods for the Preparation of Enzyme-Antibody Conjugates for use in Enzyme Immunoassay, in *Methods in Enzym.* (ed J. Langone & H. Van Vunakis), Academic press, New York, 73: 147-166 (1981).

Examples of enzyme-substrate combinations include, for example:

(i) Horseradish peroxidase (HRPO) with hydrogen peroxide as a substrate, wherein the hydrogen peroxidase oxidizes a dye precursor (e.g. orthophenylene diamine (OPD) or 3,3',5,5'-tetramethyl benzidine hydrochloride (TMB));

(ii) alkaline phosphatase (AP) with para-Nitrophenyl phosphate as chromogenic substrate; and

(iii)  $\beta$ -D-galactosidase ( $\beta$ -D-Gal) with a chromogenic substrate (e.g. p-nitrophenyl- $\beta$ -D-galactosidase) or fluorogenic substrate 4-methylumbelliferyl- $\beta$ -D-galactosidase.

Numerous other enzyme-substrate combinations are available to those skilled in the art. For a general review of these, see U.S. Patent Nos. 4,275,149 and 4,318,980.

In the assays of the present invention, a hybrid molecule is preferably bound to a solid phase support or carrier. By "solid

phase support or carrier" is intended any support capable of binding an antigen or antibodies. Well-known supports, or carriers, include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amyloses, natural and modified  
 5 celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or  
 10 antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art  
 15 will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

In a preferred embodiment, a sandwich immunoassay is employed, *i.e.*, Erb2 is detected or measured by a method  
 20 comprising binding of a first antibody or hybrid molecule to the Erb2 antigen, and binding of a second antibody or hybrid molecule to the Erb2, and detecting or measuring Erb2 immunospecifically bound by both the first and second antibody or hybrid molecule. In a specific embodiment, either the first or second antibodies  
 25 are monoclonal antibodies and either or both of the first and second are hybrid molecules of the present invention. In this embodiment, the peptide ligand portion of the hybrid molecule preferably binds to a site different from that of the first antibody (as reflected *e.g.*, by the lack of competitive  
 30 inhibition between the antibody and the hybrid molecule for

binding to the antigen). In another specific embodiment, the first or second antibody is a polyclonal antibody.

Kits comprising one or more containers or vials containing components for carrying out the assays of the present invention are also within the scope of the invention. For instance, such a kit can comprise reagents required for the immunohistochemical analysis of a sample such as a tumor biopsy. Reagents may include one or more binding partners, e.g. a hybrid molecule or an antibody. For histological assays the kit contains the chromogenic substrate as well as a reagent for stopping the enzymatic reaction when color development has occurred. The substrate included in the kit is one appropriate for the enzyme conjugated to one of the hybrid molecules of the present invention. These are well-known in the art. The kit can optionally also comprise a standard, e.g., a known amount of purified Erb2.

The following examples are offered by way of illustration and not by way of limitation. The disclosures of all citations in the specification are expressly incorporated herein by reference.

## EXAMPLES

### EXAMPLE I

Identification and Maturation of HER2 Binding Peptides  
Methods

Phage Libraries- Random sequence polyvalent peptide phage libraries (**Table 1**) were constructed using large scale Kunkel mutagenesis of the template pB2479.g8. This phagemid contains the Tac promoter the mal signal sequence, 3 stop codons and a

linker sequence fused to gVIII and includes the LacI<sup>q</sup> and  
ampicillin resistance genes. The peptide libraries are thus  
expressed polyvalently on phage as fusions to pVIII with the  
ability to regulate copy number with IPTG. Each library has a  
5 diversity in excess of 10<sup>9</sup> clones.

**Table 1**

	Sequence
<b>Pool 1</b>	X <sub>4</sub> CX <sub>2</sub> GPX <sub>4</sub> CX <sub>4</sub> X <sub>7</sub> CX <sub>4</sub> CX <sub>7</sub> X <sub>7</sub> CX <sub>5</sub> CX <sub>6</sub> X <sub>6</sub> CX <sub>6</sub> CX <sub>6</sub>
<b>Pool 2</b>	X <sub>6</sub> CX <sub>7</sub> CX <sub>5</sub> X <sub>5</sub> CX <sub>8</sub> CX <sub>5</sub> X <sub>5</sub> CX <sub>9</sub> CX <sub>4</sub> X <sub>4</sub> CX <sub>10</sub> CX <sub>4</sub>
<b>Pool 3</b>	X <sub>8</sub> X <sub>2</sub> CX <sub>2</sub> CX <sub>2</sub> X <sub>2</sub> CX <sub>3</sub> CX <sub>2</sub> X <sub>2</sub> CX <sub>4</sub> CX <sub>2</sub>
<b>Pool 4</b>	X <sub>2</sub> CX <sub>5</sub> CX <sub>2</sub> X <sub>2</sub> CX <sub>6</sub> CX <sub>2</sub> X <sub>2</sub> CX <sub>7</sub> CX <sub>2</sub>
<b>Pool 5</b>	X <sub>2</sub> CX <sub>8</sub> CX <sub>2</sub> X <sub>2</sub> CX <sub>9</sub> CX <sub>2</sub> X <sub>2</sub> CX <sub>10</sub> CX <sub>2</sub>
<b>Pool 6</b>	CCX <sub>3</sub> CX <sub>5</sub> C CCX <sub>5</sub> CX <sub>4</sub> CX <sub>4</sub> CC
<b>Pool 7</b>	CXCX <sub>7</sub> CX <sub>3</sub> CX <sub>6</sub> CX <sub>6</sub> CX <sub>6</sub> CCX <sub>3</sub> CX <sub>6</sub> C

*Selection Conditions* - HER2-ECD was immobilized directly to  
maxisorp plates in 50 mM ammonium bicarbonate, pH 9.3, using 5  
µg/ml, overnight at 4°C. Wells were blocked using PBS containing

1% BSA (PBS-BSA) for 1 hr at 25°C. The phage from the libraries described above were pooled into 7 groups as indicated in Table 1. Phage from each pool were incubated in wells containing HER2-ECD in PBS-BSA for 3 hr at 25°C; generally about  $5 \times 10^{10}$  phage were added at the beginning of each round. Unbound phage were removed by repetitive washing with PBS containing 0.05% Tween 20 (PBS-Tween); remaining phage were eluted with 500 mM KCl, 10 mM HCl, pH2. The eluted phage were then amplified in XL1-Blue cells with VCSM13 helper phage (Stratagene) overnight at 37 °C. IPTG (10 µM) was added only to the initial phage libraries and during amplification following round 1; later rounds relied on basal expression of the tac promoter for production of peptide-pVIII expression. Enrichment was monitored by titering the number of phage which bound to a target coated well compare to a well coated with BSA.

*HER2 Phage Binding Assay*- Inhibition of binding of phage displaying a single copy of peptide 1.1FI (Table 1) on their surface to the immobilized extracellular domain of Erb2 (HER2-ECD, Hudziak et al. (1991) J. Biol. Chem. 266:24109-15) was monitored using a phage ELISA. HER2-ECD was immobilized directly to Maxisorp plates (Nunc) in 50 mM ammonium bicarbonate, pH 9.3, using 5 µg/ml, overnight at 4° C. Wells were blocked using PBS containing 1% BSA (PBS-BSA) for 1 h at 25° C. Dilutions of 1.1FI-Fc in PBS-BSA were tested for their ability to block the binding of 1.1FI displaying phage to the immobilized HER2-ECD. The microtiter plate was washed with PBS containing 0.05% Tween20 (PBS-Tween) and the phage bound to HER2-ECD were detected with an anti-gVIII/HRP monoclonal antibody conjugate (Amersham Pharmacia



Biotech). The amount of HRP bound was measured using ABTS/H<sub>2</sub>O<sub>2</sub> substrate and monitoring the change at 405 nm.

## Results

### 5 Selection of Polyvalent Peptide-Phage that bind to HER2-ECD-

Polyvalent peptide libraries were sorted in 7 pools (**Table 1**) against immobilized HER2-ECD. Polyvalent phage display (Scott et al. (1990) Science 249:386-390) was used to enhance binding through avidity effects. Enrichment, the number of phage eluted from a well coated with HER2-ECD divided by the number of phage of eluted from a well coated with BSA, is shown in **Figure 4** for rounds 3 and 4. The DNA from random clones in each pool were sequenced and the deduced peptide sequences are presented in **Table 2**. Pool 1 was taken over by a single clone, while other pools contained multiple sequences.

Using a phage binding assay, phage clones 1.1, 5.1 and 7.1 were found to bind immobilized HER2-ECD, but not to immobilized BSA, or closely related HER3 or HER4 indicating they specifically recognized HER2-ECD (**Figure 5**). The sequences of these clones were subjected to partial randomization in order to re-select for higher affinity clones.

**Table 2**

clone	Sequence	SEQ ID NO:
<b>Pool 1</b>		
1.1	Y E V E A W D C M G P G C A N L F E A H	132
<b>Pool 2</b>		
2.1	S S E C A C D K G G R R V L C I N K V G	133

2.3	E P H G C S L W D W E L R T C S E Y A N	134
2.5	K E R P C A G D A P R K G V C H V A T H	135
2.6	K V R S C I E E S L D T R R C Y L V V E	136
2.7	A K T S S C G E H E E R R A V C V L S R	137
<b>Pool 3</b>		
3.1	K V W S V Q S P	138
3.2	G K V Q R C I P	139
3.3	Q T C R R V L C L P	140
3.4	R V W T W R W N	141
3.5	R I C T T P C A V	142
3.6	T S C R R V F C A V	143
3.7	R V C T G C V T	144
3.8	K V C T R V C C G T	145
<b>Pool 4</b>		
4.1	H P C H M R V L C A A	146
4.2	R G C K A T G K V L C S L	147
4.3	S G C L R A V G A C N T	148
4.4	A G C G S K A V C V S	149
4.5	R V W T A P Q C L I	150
4.6	K V C H A S S G C V A	151
4.7	R A C Q R A C L C P A	152
<b>Pool 5</b>		
5.1	R S C A D V A S R C W E H C I T	153

5.2	T D C G R V A S V C W E S C L I	154
<b>Pool 6</b>		
6.1	C C E T R W W C Q W G F C S G S A C C	155
6.2	G C K R V C S L G V M C	156
<b>Pool 7</b>		
7.1	C S W V L V Q C G G E W W H C C G L G C G L V V N A C	157
7.5	C G C E E R K A W K C Q E A C A R S G T V	158

**EXAMPLE II**

## Methods

*Partial or Complete Randomization on Monovalent Phage-* Monovalent libraries which display a single copy of a peptide on the surface of phage fused through a linker sequence to the tail protein coded for by gIII were constructed using single-stranded template-directed mutagenesis (Kunkel et al. (1991) Met. Enz. 204:125-139) of a similar phagemid pB2479.g3. In this vector the coding sequence for gVIII has been replaced by a gIII, in addition, the CMP<sup>r</sup> gene has been inserted into a unique hincII site in the AMP<sup>r</sup> gene. The change in drug resistance was designed to eliminate contamination by related although weaker affinity polyvalent clones which could take over the population through avidity effects (Cwirla et al. (1990) Proc. Natl. Acad. Sci. USA 87:6378-6382). Partially randomized libraries were designed to maintain a bias towards the peptide sequences identified from the initial polyvalent libraries while allowing a 50% mutation rate at each amino acid position. This mutation rate

was attained by synthesizing the oligos with a 70-10-10-10 mixture of bases (where each base in the doped region of the oligo is coupled using a mixture containing 70% of the base contributing to wildtype sequence and 10% each of the other 3 bases). In contrast, complete randomization in libraries was obtained by synthesizing oligos using NNS for particular codons in order to fully randomize portions of a displayed peptide while keeping other portions of the sequence constant.

## Results

*Partial Randomization of Peptide-Phage* - The initial peptide libraries that were designed encoded a potential diversity of greater than  $20^{20}$  ( $10^{26}$ ) different clones while the actual libraries that were made contained approximately only  $10^9$  clones; an incredibly small fraction of the potential diversity. In order to narrow the search and yet further explore the peptide diversity within the area of the initially selected peptides, a partial randomization technique was employed. This technique maintains a bias towards the wildtype sequence while introducing a 50 % mutation rate (at the amino acid level) at each amino acid position; thus on average, a phage displayed 20 amino acid peptide would acquire 10 random mutations. In addition, anticipation of further affinity improvements led us to construct these libraries on monovalent phage (gIII) (Bass et al., (1990) *Proteins: Struct. Funct. Genet.* 8:309; Lowman et al., (1991) *Biochemistry* 30:10832) in order to eliminate avidity effects.

Monovalent partial randomization libraries of clones 1.1, 5.1 and 7.1 were constructed and sorted for 4 rounds on HER2. Enrichment of >10,000 fold was observed for libraries 1.1 and 7.1; however,

no enrichment of library 5.1 was observed. Again, random clones were selected and sequenced; the deduced peptide sequences from clones in libraries 1.1 and 7.1 are shown in Figure 15. Several amino acid positions in libraries 1.1 and 7.1 were 100 % retained yet multiple codons were observed at many of these positions. Residues strongly retained following partial randomization may be crucial for binding either through direct contacts or for structural reasons.

*Full maturation of HER2 binding sequences* - To complete the affinity maturation of the Class 1 sequences, a third set of libraries were constructed which fixed positions that had been 100 % conserved and remaining positions were fully randomize. In addition, the role of residues flanking the disulfide loop of the Class 1 sequence was addressed by constructing libraries with either portions of the amino and carboxy terminal missing. Thus, 3 monovalent libraries were constructed as described in **Figure 16**. Enrichment of >500-fold was observed by each library by round 4; the sequences from random clones are presented in Figure 16. Even though these libraries which fully randomized up to 10 positions were far from complete, a comparison of the full length and amino terminal truncated libraries demonstrated a preference for an additional disulfide in the C terminal region of the Class 1 sequence. In both libraries the additional disulfide is found in 2 locations. In the third library, truncation of the C terminal positions preclude the selection of an additional disulfide at these locations. Aside from the selection of an additional disulfide, the residues selected at other randomized positions are quite diverse.

**EXAMPLE III**

## Methods

*Peptide Synthesis*- Peptides were synthesized by either manual or automated (Milligen 9050) Fmoc-based solid phase synthesis on a 0.25 mmol scale using a PEG-polystyrene resin (Bodanszky et al. (1984) Int. J Peptide and Protein Res. 23(1):111) . Side chain protecting groups were removed and the peptide was cleaved from the resin with 95 % trifluoroacetic acid (TFA) and 5 % triisopropylsilane. A saturated iodine solution in acetic acid was added to oxidation of disulfide bonds. Peptides were purified by reversed-phase HPLC using a water/acetonitrile gradient containing 0.1 % TFA. Peptides were >95 % pure by analytical HPLC and its identity verified by mass spectrometry.

*Production of peptide-Z fusions* - Phage peptides selected for binding to HER2-ECD were expressed and secreted from *E. coli* (27C7) as fusions to the Z domain from protein A. Oligos were designed to insert the coding sequence for the phage-peptide sequences between the stII signal sequence and the Z domain in a plasmid containing the Z domain (pZCT). Cells were grown in phosphate limiting media and peptide-Z fusions were purified from the media using an IgG affinity column as described (Dennis et al., (1993) Proteins: Struct. Funct. Genetics 15:312-321). IgG affinity purified peptide Z-fusion was biotinylated using NHS-LC-biotin (Pierce) and characterized by mass spectrometry. Peptide-Z fusions which formed multimers could be separated into monomer and dimer containing fractions by size exclusion chromatography on a Superdex 75 column in PBS.

*Removal of the Z domain from purified peptide-Z fusions* - Removal of the Z domain from purified peptide-Z fusions was accomplished by digestion of the fusion with trypsin. Trypsin (1 %, w/w) was added for 4 hrs at 37°C in 100 mM Tris pH 8.0 and 10 mM CaCl<sub>2</sub>.

5 The peptide, free of the Z domain was then purified on a C18 reverse-phase HPLC column using a 20 to 50 % acetonitrile gradient in 0.1 % TFA.

10 *Construction of Her2-Fc expression vector*-Standard recombinant DNA techniques were used for the construction of a recombinant transfer vector based on the vector pVL1393 (Pharmigen) (Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989) *Molecular Cloning: A Laboratory Manual*, second Ed., Cold Spring Harbor Laboratory Press, New York; O'Reilly, D. R., Miller, L. K., and Luckow, V. A. (1994) *Baculovirus Expression Vectors: A Laboratory Manual*, Oxford University Press, New York). The pVL1393 derived plasmid pbPH.His was linearized with *Nco* I and *Sma* I and treated with shrimp alkaline phosphatase (Dwyer, M. A. et al. (1999) J. Biol. Chem. 274:9738-9743). The Fc portion of the human IgG1 was 20 obtained as a 700 base pair fragment by restriction digestion using *Nde* I and subsequent treatment with Klenow and *Nco* I of another pVL1393 derived plasmid pVL1393.IgG. The signal sequence for MIP.5 was introduced before the Fc sequence as a PCR fragment digested with *EcoR* I, included within the fragment is an *Asc* I 25 site. The *Asc* I site occurs following the putative signal sequence cleavage site. Following ligation, competent *E. coli* XL-1 Blue were transformed and bacteria were selected for the correct recombinant plasmid (pVL1393.MIP.5sig.Fc) by DNA sequence analysis. Then, pVL1393.MIP.5sig.Fc was linearized with *Asc* I 30 and *Stu* I and treated with shrimp alkaline phosphatase. The

linearized vector was then ligated with a synthetic piece of DNA with compatible ends. The synthetic DNA insert was formed by annealing 2 oligos with the sequences: 5'-CGC GCC CAG GTG TAC GAG TCC TGG GGA TGC ATC GGC CCC GGC TGC GCC TGC CTG CAG GCC TGC CTG GGA GGC GGG AGC TCC GGC-3' (SEQ ID NO:159) and 5'-GCC GGA GCT CCC GCC TCC CAG GCA GGC CTG CAG GCA GGC GCA GCC GGG GCC GAT GCA TCC CCA GGA CTC GTA CAC CTG GG-3' (SEQ ID NO:160) coding for peptide sequence 1.1FI including a GGGSSG (SEQ ID NO:130) linker. Following ligation, competent *E. coli* XL-1 Blue were transformed and bacteria were selected for the correct recombinant plasmid (termed pVL.1393.MIP5.1.1FI-Fc) by DNA sequence analysis using the dRhodamine dye-terminator method and an Applied Biosystems ABI Model 373 automated DNA sequencer. Recombinant transfer vector was purified using a Qiagen Mini-Prep and used for construction of recombinant baculovirus.

Recombinant baculovirus was generated following cotransfection of Sf9 cells with the transfer vector and the linearized wild type baculovirus DNA (*Autographa californica* nuclear polyhedrosis virus (AcNPV), Pharmingen). A primary amplification of the recombinant baculovirus achieved detectable protein expression. Subsequent plaque-purification and titering of the viral stock was performed by plaque assays. Standard methods were utilized as previously described (O'Reilly, D. R., Miller, L. K., and Luckow, V. A. (1994) *Baculovirus Expression Vectors: A Laboratory Manual*, Oxford University Press, New York).

*Cell Culture*—Adherent cultures of *Spodoptera frugiperda* (Sf9) insect cells (ATCC CRL 1711) were maintained at 28 °C in Hink's TNM-FH insect medium supplemented GRACE's (JRH Biosciences, #51942-78P), with glutamine, streptomycin/penicillin, and 10% fetal bovine serum (heat



inactivated for 30 min at 56 °C). Cultures were passaged every 3 days. Spinner cultures of High 5 cells (*Trichoplusia ni*, BT1.TN.SB1-4 (Invitrogen)) (500 ml at  $2.0 \times 10^6$  cells/ml) were infected at a multiplicity of infection of 0.5 and harvested 60 h posttransfection. Suspension cultures were maintained in spinner flasks at 28 °C using ESF-921 protein free insect cell culture medium (Expression Systems LLC, #96-001). Cultures were passaged every 3 days to a starting cell density of  $10^6$  cells/ml.

*Peptide-Fc Purification*—Following the optimized infection protocol, the High 5 cells were removed by centrifugation at 800 x g at 4 °C for 10 min. The clarified supernatant (0.5 L) was filtered using a 0.45 µ Nalgene filter and applied to a 0.5 ml Hi-Trap Protein A Column (Amersham Pharmacia Biotech) equilibrated with PBS (phosphate buffered saline) at 25 °C. After washing with 20 ml of PBS, the column was eluted with 3 ml of 0.2 N HOAc and fractions containing peptide-Fc were lyophilized and stored at 4 °C.

*SDS-PAGE* —Samples were analyzed reduced and unreduced on a 4-20% Tris-glycine SDS-PAGE (Novex) along with prestained protein molecular weight markers (SeaBlue, Novex) using the method of Laemmli (Laemmli, U. K. (1970) Nature 227:680-685).

*Protein Sequencing*— 1.1FI-Fc purified from the infected Sf9 cell supernatants was subjected to SDS-PAGE, and then transferred to a PVDF membrane. Electroblothing onto Millipore Immobilon-PSQ membranes was carried out for 1 h at 250 mA constant current in a BioRad Trans-Blot transfer cell (Matsudaira, P. (1987) J. Biol. Chem. 262: 10035-10038). The PVDF membrane was stained with 0.1% Coomassie Blue R-250 in 50% methanol, 0.5 min and destained for 2-3 min with 10% acetic acid in 50% methanol. The membrane was thoroughly washed with water and allowed to dry before storage at

-20 °C. The 1.1FI-Fc band at about 50 kD was cut out and the first 11 residues were sequenced using a model 494A Applied Biosystems sequencer equipped with an on-line PTH analyzer. Peaks were integrated with Justice Innovation software using Nelson  
5 Analytical 760 interfaces. Sequence interpretation was performed on a DEC alpha (Henzel, W. J., Rodriguez, H., and Watanabe, C. (1987) J. Chromatog. 404: 41-52).

*HER2 Competition ELISA*- 1.1FI-Fc binding to HER2-ECD was monitored using a competition ELISA. Samples were titrated in  
10 PBS-BSA and tested for their ability to block the binding of 40 nM biotinylated 1.1.FI-Z to HER2-ECD immobilized on microtiter plates as described above. Following a 1 h incubation the plate was washed with PBS-Tween and Streptavidin/HRP conjugate (Streptavidin-POD, Roche Molecular Biochemicals) was added for 30  
15 min. Plates were washed again with PBS-Tween and the bound HRP was assayed using ABTS/H<sub>2</sub>O<sub>2</sub> substrate (Kirkegaard & Perry Laboratories) and the absorbance at 405 nm was monitored. The absorbance at 405 nm was plotted versus the concentration of 1.1FI-Fc originally added to the well. Sigmoidal curves were fit  
20 to a four parameter equation by nonlinear regression analysis (Marquardt, J. Soc. Indust. Appl. Math. 11:431-441 (1963); the concentration of 1.1FI-Fc required to give a half-maximal signal in the assay was calculated from the curves and is referred to as the IC<sub>50</sub> value.

*Cell binding*- Cells expressing HER2 (BT 474 [3+], MDA 361 [2+], and BaF3 [0+]) were detached with trypsin, washed twice with Wash Buffer (PBS containing 0.5% BSA, 1 mM NaOH), and split into fractions containing 0.5 x 10<sup>6</sup> cells each. The cells were  
25 suspended in Wash Buffer containing 0, 0.5 or 5 µM 1.1.FI-Zb, washed twice with Wash Buffer and suspended in Wash Buffer  
30

containing strepavidin-PE, washed twice with Wash Buffer and subjected to FACS analysis.

## Results

5 *Characterization of Peptides that bind to HER2-ECD* - Peptide HER201 was synthesized corresponding to partially randomized phage-clone 1.1.2 (Figure 15). In addition, peptide HER212 corresponding to a representative clone 1.1.FI (Figure 16) derived from the fully randomized full length library was also  
10 synthesized. Due to the presence of 2 disulfides in this peptide, orthogonal protecting groups were used for the cysteines in order to induce a 1-2 and 3-4 disulfide arrangement. This arrangement was suspected because of the order in which the disulfide bonds evolved during the selection process.

15 Additionally, this peptide and a peptide sequence derived from the consensus of library 7.1 (Figure 15) (7.1c) were expressed and secreted from *E. coli* as a fusion to the Z domain of protein A (called 1.1.FI-Z and 7.1c-Z) where cysteine oxidation might be allowed to occur as it does during phage production. The 1.1.FI-Z preparation was biotinylated (1.1.FI-Zb) and bound to immobilized HER2 with an EC50 of 2 nM based on the total protein  
20 concentration (**Figure 6**) and served as a reagent for the competition ELISA.

25 Peptides HER201, HER212 as well as the recombinant peptide fusions 1.1.FI-Z and 7.1c-Z were tested for the ability to block binding of 1.1.FI-Zb to immobilized HER2 (**Figure 7**). HER201 and 7.1c-Z had IC50s of 300 and 1,100 nM respectively. Interestingly,  
30 HER212 and 1.1.FI-Z, which were derived from the same phage-

peptide sequence had dramatically different IC50s: 9  $\mu$ M and 50 nM respectively. One explanation could be that another disulfide arrangement was forced in the synthesis of HER212. Additionally, SDS-PAGE analysis of 1.1.FI-Z (**Figure 8B**) (lane S) revealed a heterogeneous mixture likely due to multimerization caused by intermolecular disulfides. Mass spectral analysis confirmed presence of dimer 1.1.FI-Z while HER212 was present only as monomer.

The 1.1.FI-Z preparation was further purified using a Superdex 75 into monomer and dimer containing fractions (**Figure 8A and 8B**). Surprisingly, HER2 binding activity coincided with the dimer fractions rather than the monomer fractions (**Figure 8B and 8C**) when assayed in the HER2 competition ELISA.

In addition, 1.1.FI-Z was digested with trypsin to removed the Z domain and subjected to reversed phase HPLC. Fractions from the HPLC were tested for their ability to compete in the HER2 competition ELISA. The active fraction had a mass corresponding to the sequence of HER212 but was also found to contain dimer. This fraction had an IC50 of 3 nM in the HER2 competition ELISA based on protein concentration.

In an attempt to facilitate dimer formation, an expression vector was constructed in which the amino acid sequence of 1.1.FI was repeated twice prior to fusion with Z domain (**Figure 9**). While this "single chain dimer" (called (FI)<sub>2</sub>-Z), also produced dimer when expressed, the dominate species formed was monomer (**Figure 9B**). In addition, when fractionated on a Superdex 75 column (**Figure 9A**) and assayed in the HER2 competition ELISA, the active species was now identified as monomer (**Figure 9B and C**). (FI)<sub>2</sub>-Z

has a similar affinity for HER2 as the 1.1.FI-Z dimer ( $IC_{50} = 20$  nM).

*Binding Site on HER2* - To test whether Class 1 and Class 7 sequences bound to the same or independent sites on HER2, the binding of phage clones from Class 1 and Class 7 libraries to immobilized HER2 was examined in the presence of HER201 or 7.1c-Z. From **Figure 10A and 10B**, it is apparent that HER201 and 7.1c-Z block the binding of both Class 1 and Class 7 phage suggesting that both Classes bind to the same site on HER2. A closer look at the sequences obtained in these 2 classes reveals a core homology region (**Figure 11**).

The binding site of the Class 1 and Class 7 peptides also appears to be a novel site on HER2 in that known monoclonal antibodies to HER2 did not directly compete with 1.1.FI-phage binding to immobilized HER2 (**Figure 12**). Increasing concentrations of various monoclonal antibodies were added to block 1.1.FI-phage binding to immobilized HER2 without effect. The reduction in binding at very high concentrations of 3H4 ( $>100$  nM) are thought to result through an indirect effect since the affinity of this monoclonal antibody for HER2 is below 100 pM.

*Cell Binding* - 1.1.FI-Zb was tested for its ability to recognize HER2 expressed on cells. Three cell types which expressed HER2 at different levels were examined: BT 474 [3+] ( $3 \times 10^6$  receptors/cell), MDA 361 [2+] ( $4 \times 10^5$  receptors/cell), and a control cell line that doesn't express HER2, BaF3. By FACS analysis, 1.1.FI-Zb was found to bind to cells proportional to the number of HER2 of receptors expressed/cell and the

concentration of 1.1.FI-Zb used (**Figure 13**).

*Peptide-Fc fusions* - DNA coding for the 1.1.FI sequence was fused through a linker to an Fc from a IgG<sub>1</sub> and expressed in baculovirus. The resulting protein was purified on a Protein A column and characterized under oxidizing and reducing conditions by SDS-PAGE (**Figure 14**). A clear molecular weight shift is observed under these 2 conditions suggesting dimerization of the Fc. This molecule, when tested for its ability to block 1.1FI phage binding to immobilized HER2, has an IC<sub>50</sub> of 3 nM. When tested in the HER2 competition ELEISA, 1.1FI-Fc had a similar IC<sub>50</sub> to 1.1FI-Z indicating that the 1.1FI sequence was fully capable of binding HER2 when fused to an Fc (Figure 17).

WHAT IS CLAIMED IS:

1. A non-naturally occurring peptide ligand which competes for binding HER2 in an in vitro assay with a peptide ligand having the formula:

Xaa<sub>(1-14)</sub>-Cys-Xaa<sub>16</sub>-Gly-Pro-Gly-Cys-Xaa<sub>(21-27)</sub> (SEQ ID NO:90)  
wherein X<sub>(1-14)</sub> is absent or between one and fourteen amino acids; Xaa<sub>16</sub> is an amino acid selected from the group consisting of Met, Thr, Cys and Ile and Xaa<sub>(21-27)</sub> is absent or between one and 7 amino acids.

2. The peptide ligand of claim 1 having the following formula:

Xaa<sub>(1-7)</sub>-Cys-Xaa<sub>9</sub>-Gly-Pro-Gly-Cys-Xaa<sub>(14-20)</sub> (SEQ ID NO:92)  
wherein X<sub>(1-7)</sub> is absent or between one and seven amino acids; and Xaa<sub>9</sub> is an amino acid selected from the group consisting of Met, Ile, Thr or Cys and Xaa<sub>(14-20)</sub> is absent or between one and seven amino acids.

3. The peptide ligand of claim 2 having the following formula:

Xaa<sub>(1-7)</sub>-Cys-Ile-Gly-Pro-Gly-Cys-Xaa<sub>(14-20)</sub> (SEQ ID NO:161).

4. A peptide ligand having the formula A-A wherein A is the peptide ligand of claim 3 and "-" is an optional linker domain.

5. The peptide ligand of claim 3 having the following formula:

Xaa<sub>(1-5)</sub>-Trp-Gly-Cys-Ile-Gly-Pro-Gly-Cys-Xaa<sub>(14-20)</sub> (SEQ ID NO:93)

wherein Xaa<sub>(1-5)</sub> is absent or between one and five amino acids.

6. The peptide ligand of claim 5 having the following formula:

wherein Xaa<sub>(1-3)</sub> is absent or between one and three amino acids,  
Xaa<sub>5</sub> is an amino acid,  
Xaa<sub>5</sub> is an amino acid,  
Xaa<sub>14</sub> is an amino acid,  
Xaa<sub>19</sub> is an amino acid and  
-Xaa<sub>(17-20)</sub> is absent or between one and four amino acids.

Gln-Arg-Asn-  
Leu-Ser-Pro-  
Glu-Asn-Trp-  
Ala-Ser-His-  
Lys-Leu-Asn-  
Thr-Gln-Ala-  
Ala-Pro-Arg-  
Gln-Val-Tyr-  
Arg-Thr-Glu-  
Phe-Ala-Gly-  
Thr-Ala-Arg-  
Arg-Pro-His-  
Asn-Val-Cys-  
Cys-Ile-Asp-  
Tyr-Glu-Trp-  
Arg-Trp-Asp-  
His-Trp-Met-  
Asn-Trp-Pro-  
Phe-Asn-Trp-



Phe-Ser-Gly-  
Gly-Gly-Trp-  
Leu-Trp-Phe-  
Gly-Ile-Pro-  
Trp-Trp-Thr-  
Leu-Gly-Trp-  
Ser-Pro-Trp-  
Arg-Gly-Trp-,

Xaa<sub>5</sub> is selected from the group consisting of:

Ala, Thr, Met, Val, Arg, Glu, Asp, Ser, Gln, Pro, Gly, Phe and  
Lys,

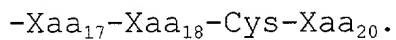
Xaa<sub>14</sub> is selected from the group consisting of:

Glu, Lys, Arg, Asp, Ser, Ala, Asn, Gly, Pro and Gln,

Xaa<sub>15</sub> is selected from the group consisting of:

Met, Phe, Ala, Met, Cys, Gln, Glu, Ala, Trp, Phe, Leu, Val, Tyr,  
Trp, and

-Xaa<sub>(17-20)</sub> is a four amino acid peptide having the following  
formula:



8. The peptide ligand of claim 7 wherein -Xaa<sub>(17-20)</sub> is selected  
from the group consisting of:

-Gln-Ala-Cys-Met (SEQ ID NO:102)  
-Leu-Gln-Cys-Trp (SEQ ID NO:103)  
-Met-Ser-Cys-Val (SEQ ID NO:104)  
-Leu-Arg-Cys-Ile (SEQ ID NO:105)  
-Gln-Ala-Cys-Leu (SEQ ID NO:106)  
-Leu-Ser-Cys-Leu (SEQ ID NO:107)  
-Ile-Gly-Cys-Leu (SEQ ID NO:108)  
-Leu-Ala-Cys-Leu (SEQ ID NO:109)

-Leu-Ser-Cys-Ile (SEQ ID NO:110)  
-Met-Asn-Cys-Leu (SEQ ID NO:111)  
-Leu-Arg-Cys-Leu (SEQ ID NO:112)  
-Leu-Lys-Cys-Leu (SEQ ID NO:113)  
-Leu-Gly-Cys-Leu (SEQ ID NO:114)  
-Leu-Asn-Cys-Ile (SEQ ID NO:115)  
-Met-Gly-Cys-Leu (SEQ ID NO:116) and  
-Met-Ala-Cys-Leu (SEQ ID NO:117).

9. The peptide ligand of claim 6 wherein -Xaa<sub>(17-20)</sub> is a four amino acid peptide having the following formula

-Cys-Xaa<sub>18</sub>-Xaa<sub>19</sub>-Cys

wherein Xaa<sub>18</sub> is an amino acid and Xaa<sub>19</sub> is an amino acid.

10. The peptide ligand of claim 9 wherein -Xaa<sub>(17-20)</sub> is selected from the group consisting of:

-Cys-Ala-Trp-Cys (SEQ ID NO:118)  
-Cys-Ser-Trp-Cys (SEQ ID NO:119)  
-Cys-Glu-Pro-Cys (SEQ ID NO:120)  
-Cys-Asp-Trp-Cys (SEQ ID NO:121)  
-Cys-Glu-Trp-Cys (SEQ ID NO:122)  
-Cys-Asn-Trp-Cys (SEQ ID NO:123) and  
-Cys-Gly-Trp-Cys (SEQ ID NO:124).

11. The peptide ligand of claim 1 having the formula:

Xaa<sub>(1-10)</sub>-Glu-Xaa<sub>12</sub>-Trp-Xaa<sub>14</sub>-Cys-Cys-Gly-Pro-Gly-Cys-Xaa<sub>21</sub>-Xaa<sub>22</sub>-Xaa<sub>23</sub>-Xaa<sub>(24-27)</sub> (SEQ ID NO:126)

wherein Xaa<sub>(1-10)</sub> is absent or between 1 and 10 amino acids;  
Xaa<sub>12</sub> is an amino acid;

Xaa<sub>14</sub> is an amino acid;

Xaa<sub>21</sub> is an amino acid;

Xaa<sub>22</sub> is an amino acid;

Xaa<sub>23</sub> is an amino acid selected from the group consisting of Val and Leu and

Xaa<sub>(24-27)</sub> is absent or between one and four amino acids.

12. The peptide ligand of claim 11 wherein Xaa<sub>(1-10)</sub> is a 10 amino acid peptide having the following formula:

-Cys-Xaa<sub>(2-7)</sub>-Cys-Xaa<sub>9</sub>-Gly-; Xaa<sub>(24-27)</sub> is a four amino acid peptide having the following formula:

Xaa<sub>(24-26)</sub>-Cys

wherein Xaa<sub>(2-7)</sub> is a six amino acid peptide and

Xaa<sub>(24-26)</sub> is a 3 amino acid peptide.

13. A peptide ligand having the formula B-B wherein B is the peptide ligand of claim 12 and wherein "-" is an optional linker domain.

14. A peptide ligand having the formula A-B wherein A is the peptide ligand of claim 2 and B is the peptide ligand of claim 11 and wherein "-" is an optional linker domain.

15. The peptide ligand of claim 12 wherein Xaa<sub>(1-10)</sub> has the following formula:

Cys-Xaa<sub>2</sub>-Trp-Val-Xaa<sub>5</sub>-Xaa<sub>6</sub>-Xaa<sub>7</sub>-Cys-Xaa<sub>9</sub>-Gly- (SEQ ID NO:127).

16. The peptide ligand of claim 15 wherein Xaa<sub>(1-10)</sub> has the following formula:

Cys-Xaa<sub>2</sub>-Trp-Val-Xaa<sub>5</sub>-Xaa<sub>6</sub>-Xaa<sub>7</sub>-Cys-Xaa<sub>9</sub>-Gly- (SEQ ID NO:127).

and Xaa<sub>2</sub> is an amino acid selected from the group consisting of Ala and Ser;

Xaa<sub>5</sub> is an amino acid selected from the group consisting of Ser, Leu, Ala, Arg and Val;

Xaa<sub>6</sub> is an amino acid selected from the group consisting of Phe, Val and Leu;

Xaa<sub>7</sub> is an amino acid selected from the group consisting of Asp, Gln, Tyr, Trp, Leu and His and

Xaa<sub>9</sub> is an amino acid selected from the group consisting of Gly, Phe and Leu.

17. The peptide ligand of claim 16 wherein Xaa<sub>(1-10)</sub> has the following formula:

Cys-Ser-Trp-Val-Leu-Xaa<sub>6</sub>-Xaa<sub>7</sub>-Cys-Gly-Gly- (SEQ ID NO:162).

18. The peptide ligand of claim 17 wherein Xaa<sub>(24-26)</sub> has the following formula:

Xaa<sub>24</sub>-Xaa<sub>25</sub>-Xaa<sub>26</sub> and

Xaa<sub>24</sub> is an amino acid selected from the group consisting of Trp, Val, Gly and Ala;

Xaa<sub>25</sub> is an amino acid selected from the group consisting of Asn, Lys, Asp, Glu and His and

Xaa<sub>26</sub> is an amino acid selected from the group consisting of Ala, Ser and Val.

19. The peptide ligand of claim 17 wherein Xaa<sub>(24-26)</sub> has the following formula:

Xaa<sub>24</sub>-Xaa<sub>25</sub>-Xaa<sub>26</sub> and

Xaa<sub>24</sub> is an amino acid selected from the group consisting of Trp, Val, Gly and Ala;

Xaa<sub>25</sub> is an amino acid selected from the group consisting of Asn, Lys, Asp, Glu and His and

Xaa<sub>26</sub> is an amino acid selected from the group consisting of Ala, Ser and Val.

20. The peptide ligand of claim 19 wherein

Xaa<sub>24</sub> is Val;

Xaa<sub>25</sub> is Asn and

Xaa<sub>26</sub> is Ala.

21. A polypeptide which comprises:

(a) a peptide ligand according to any of claims 1, 4, 11, or 13 and

(b) an immunoglobulin constant region sequence.

22. The polypeptide of claim 21 further comprising a linker sequence.

23. The polypeptide of claim 20 or 21 wherein the immunoglobulin constant region sequence is the constant domain of an IgG heavy chain.

24. The polypeptide of claim 22 wherein said constant region sequence comprises the CH3 domain of an immunoglobulin heavy chain.

25. The polypeptide of claim 24 further comprising the hinge region of an immunoglobulin heavy chain.

26. The polypeptide of claim 25 wherein said constant region sequence comprises at least functionally active hinge, CH2 and CH3 domains of the constant region of an immunoglobulin heavy chain.

27. The polypeptide of claim 21 further comprising an additional functional moiety.

28. The polypeptide of claim 27 wherein the additional functional moiety is selected from the group consisting of a cytotoxic agent and an enzyme.

29. The polypeptide of claim 27 wherein the additional functional moiety is a cytotoxic agent.

30. A pharmaceutical composition comprising the peptide ligand of claim 1 and pharmaceutically acceptable excipient.

31. A pharmaceutical composition comprising the polypeptide of claim 21 and a pharmaceutically acceptable excipient.

32. A pharmaceutical composition comprising the polypeptide of claim 28 and a pharmaceutically acceptable excipient.

33. An isolated DNA molecule encoding the peptide ligand of claim 1.

34. The DNA molecule of claim 33 further comprising an expression control sequence operably linked to the DNA molecule.

35. An expression vector comprising the DNA molecule of claim 33 wherein the control sequence is recognized by a host cell transformed with the vector.

36. A host cell transformed with the vector of claim 35.

37. A method for expressing a DNA molecule encoding a peptide ligand in a host cell, comprising culturing the host cell of claim 36 under conditions suitable for expression of the peptide ligand.

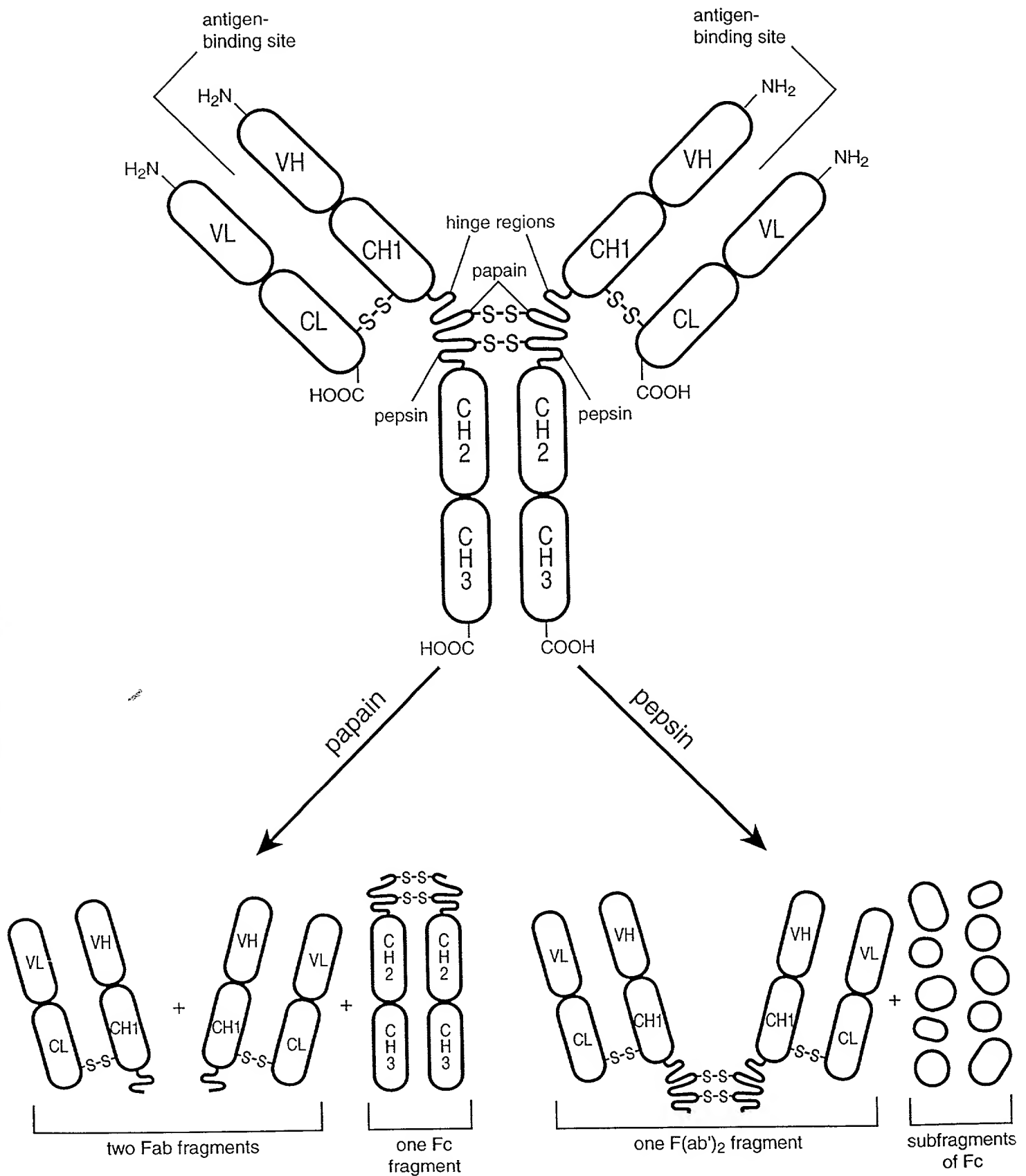
38. The method of claim 37 further comprising recovering the peptide ligand from the culture medium.

**Compounds that Bind HER2**

**Abstract of the Disclosure**

5           The invention provides novel compounds which bind to the  
human erbB2 gene product (ErbB2, also known as HER2, or c-ErbB-  
2). In particular aspects, the invention provides for the  
treatment of disorders characterized by the overexpression of  
ErbB2 utilizing the novel compounds of the invention. The  
10          invention also provides pharmaceutical compositions comprising  
the novel compounds as well as for their use in research,  
diagnostic, therapeutic, and prophylactic methods.







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 170. **Список узлов**  
 171. **Список агрегатов**  
 172. **Список систем**  
 173. **Список сетей**  
 174. **Список баз данных**  
 175. **Список программ**  
 176. **Список документов**  
 177. **Список таблиц**  
 178. **Список рисунков**  
 179. **Список формул**  
 180. **Список терминов**  
 181. **Список источников**  
 182. **Список документов**  
 183. **Список материалов**  
 184. **Список оборудования**  
 185. **Список инструментов**  
 186. **Список расходных материалов**  
 187. **Список вспомогательных материалов**  
 188. **Список запасных частей**  
 189. **Список комплектующих**  
 190. **Список деталей**  
 191. **Список узлов**  
 192. **Список агрегатов**  
 193. **Список систем**  
 194. **Список сетей**  
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 206. **Список инструментов**  
 207. **Список расходных материалов**  
 208. **Список вспомогательных материалов**  
 209. **Список запасных частей**  
 210. **Список комплектующих**  
 211. **Список деталей**  
 212. **Список узлов**  
 21

Fig. 2B

Fig. 2B



Figure 4

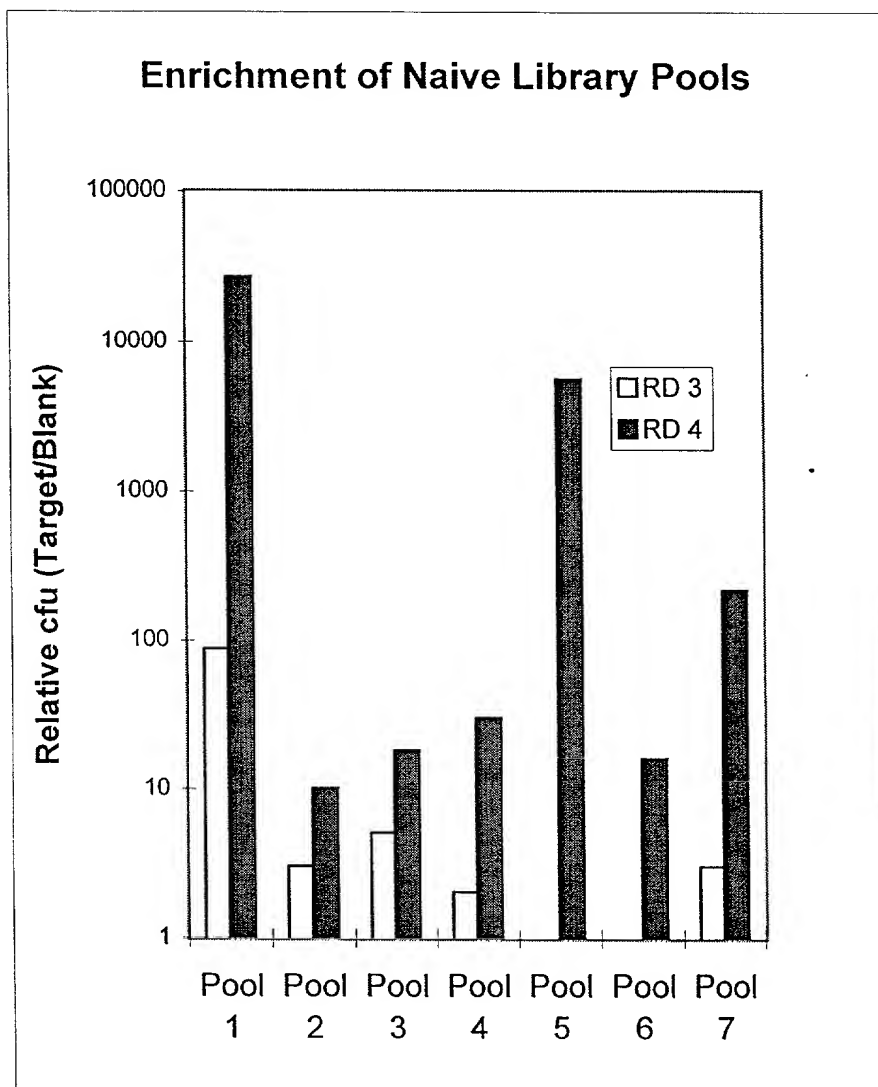
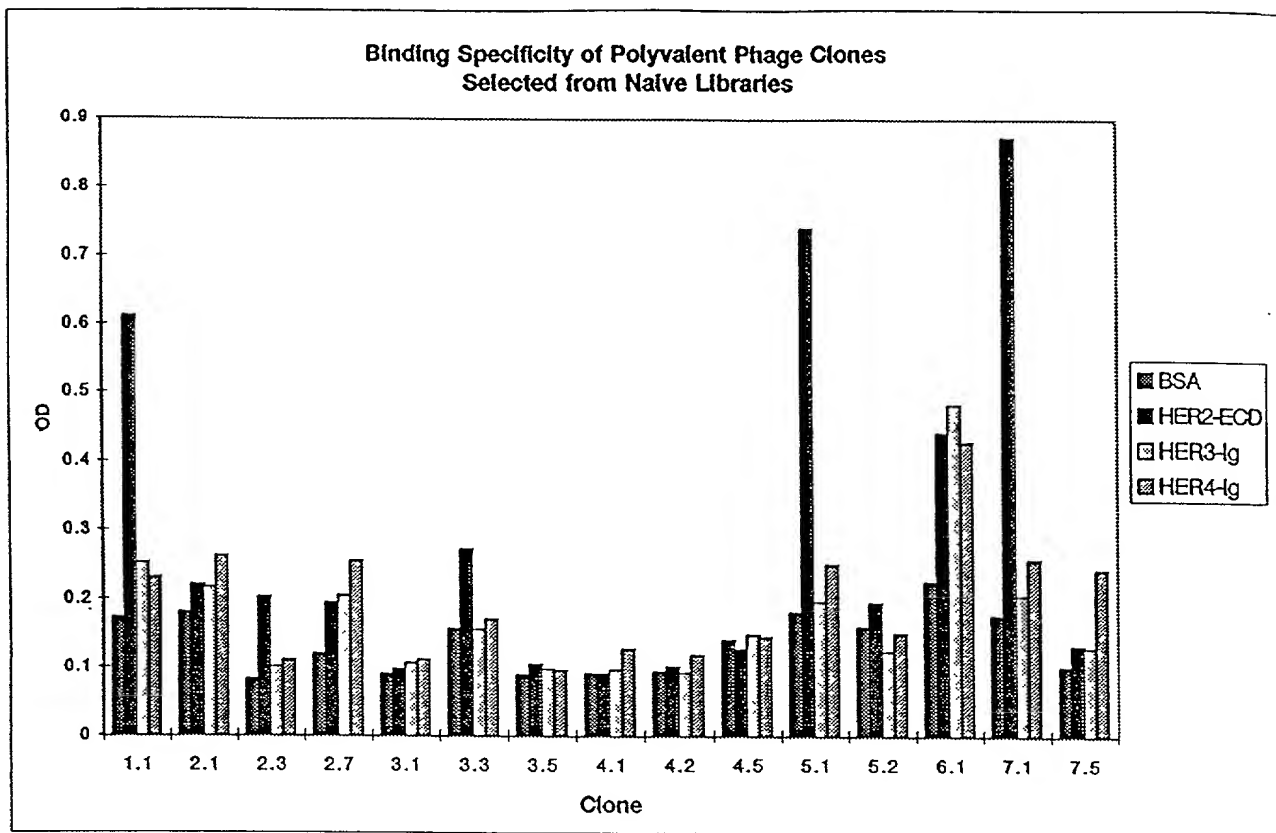


Figure 5



000000-12260960

Figure 6.

$EC_{50}$  for 1.1.FI-Zb Binding to Immobilized HER2

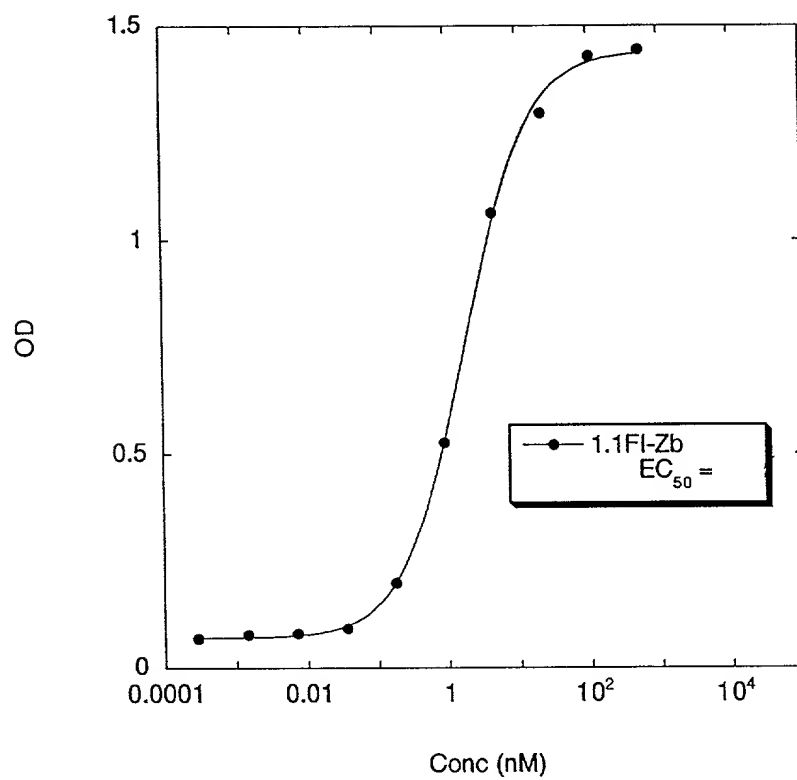


Figure 2

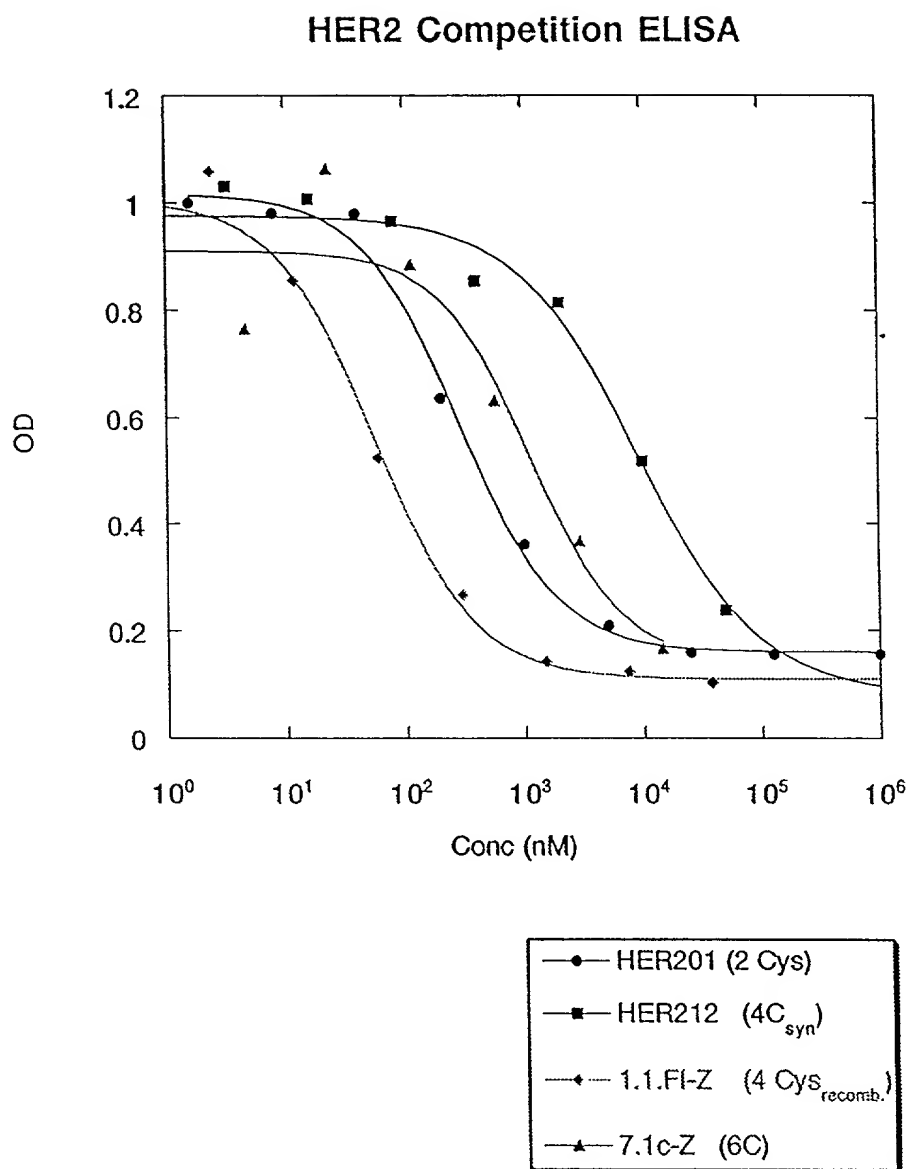


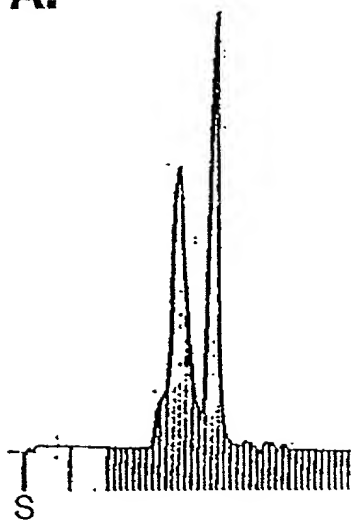


Figure 8

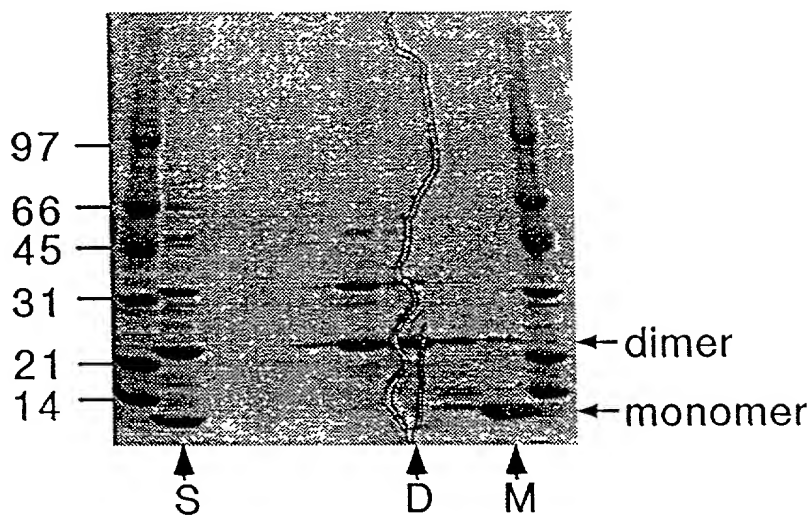
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QVYESWGCIGPGCACLQACL-Z

A.



B.



C.

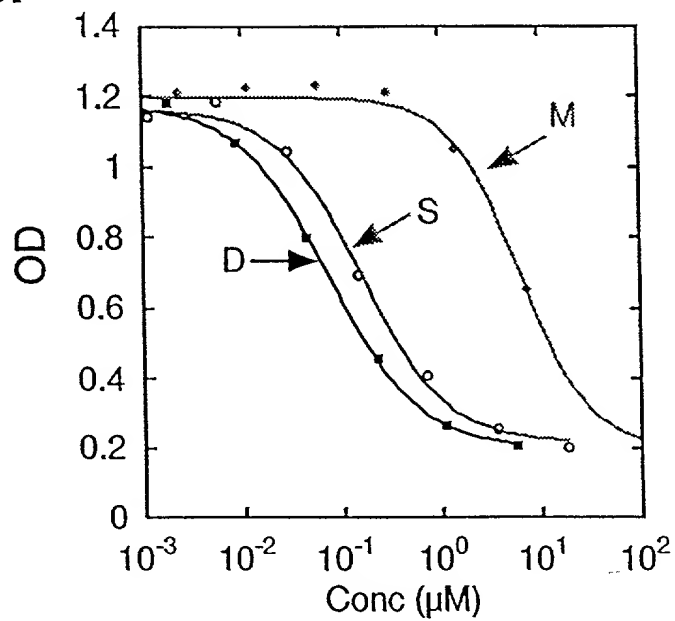
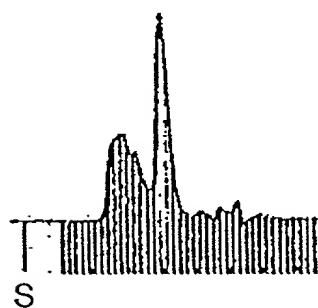


Figure 9

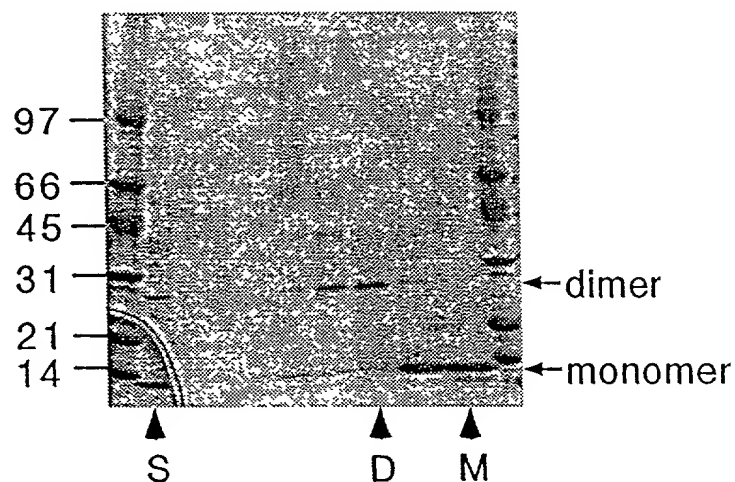
(1.1.FI)<sub>2</sub>-Z

QVYESWGCIGPGCACLQACLGGGSGGQVYESWGCIGPGCACLQACL-Z

A.



B.



C.

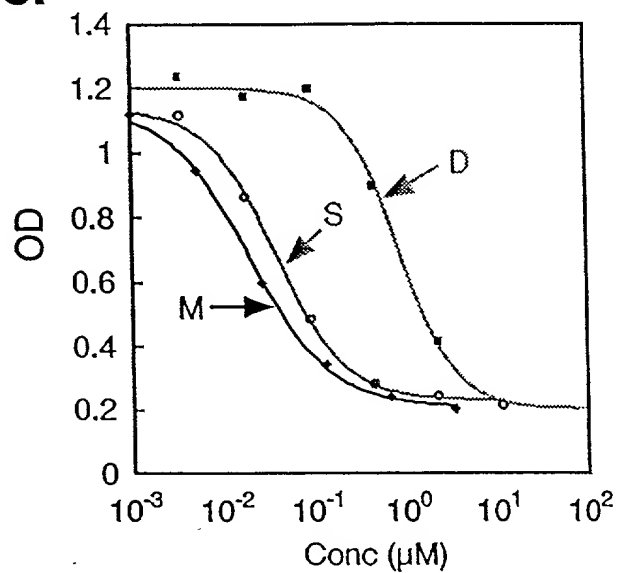
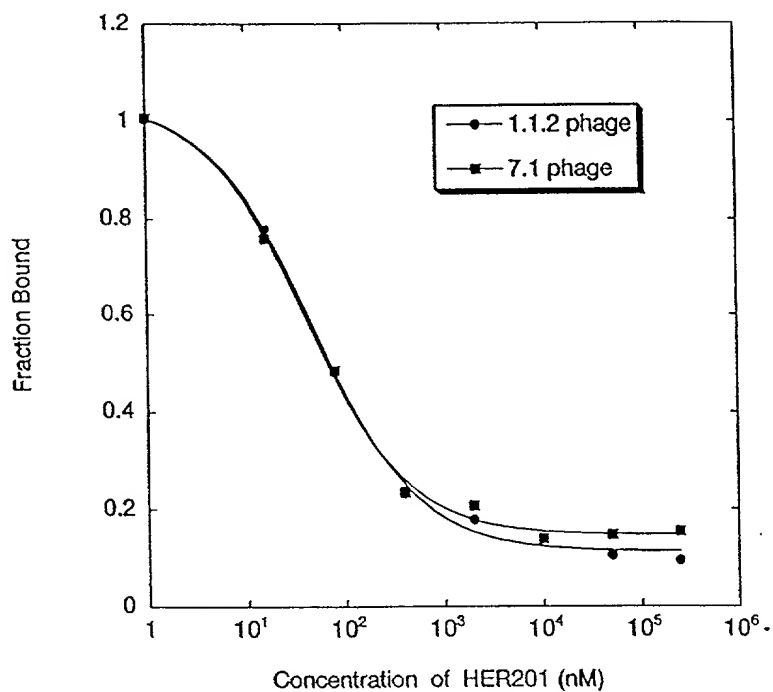
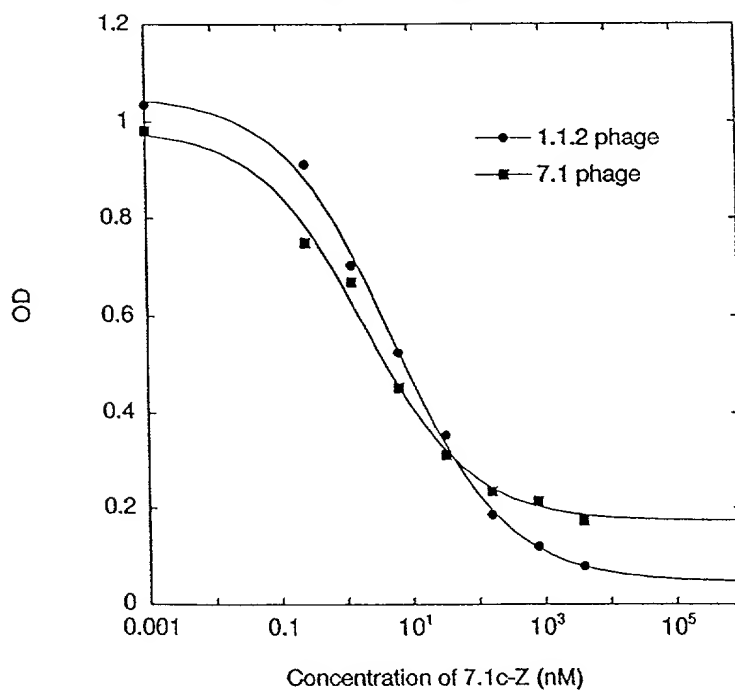


Figure 10

**Class 1 and 7 Phage binding to HER2 is blocked by HER201 peptide**



**Class 1 and 7 Phage binding to HER2 is blocked by Peptide 7.1c-Z**



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## Class 7

**Class 1**

### Class 1

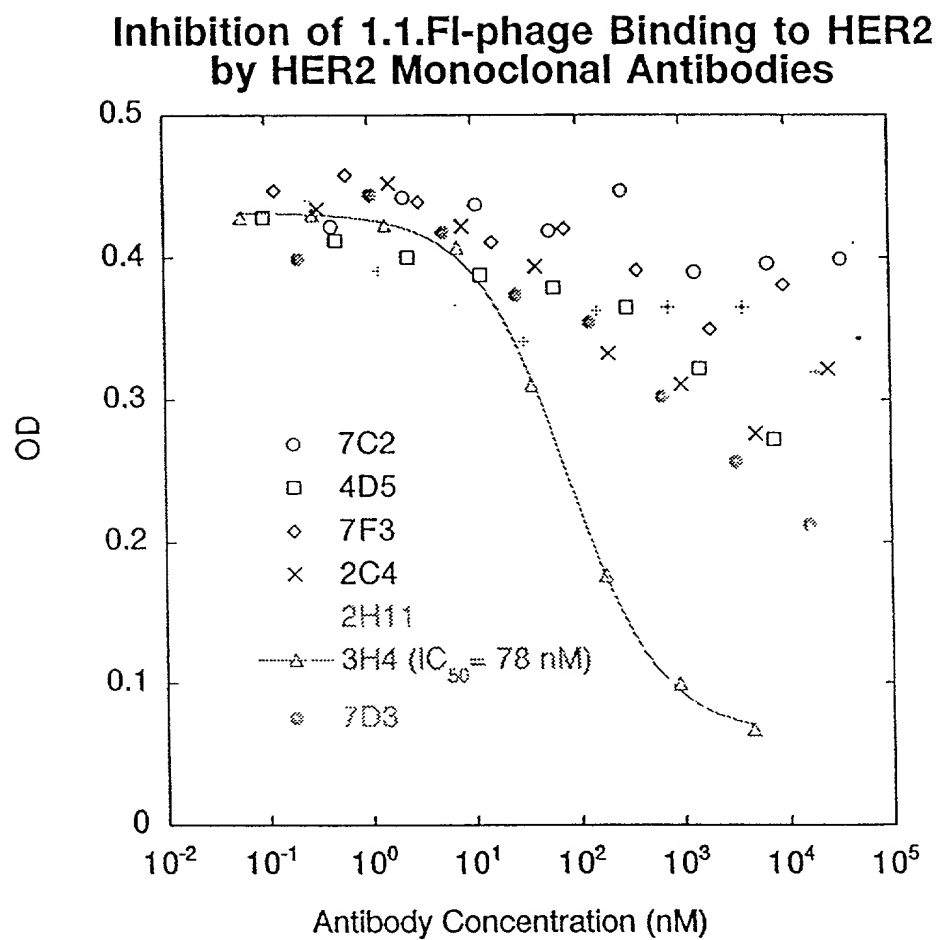
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Figure 13

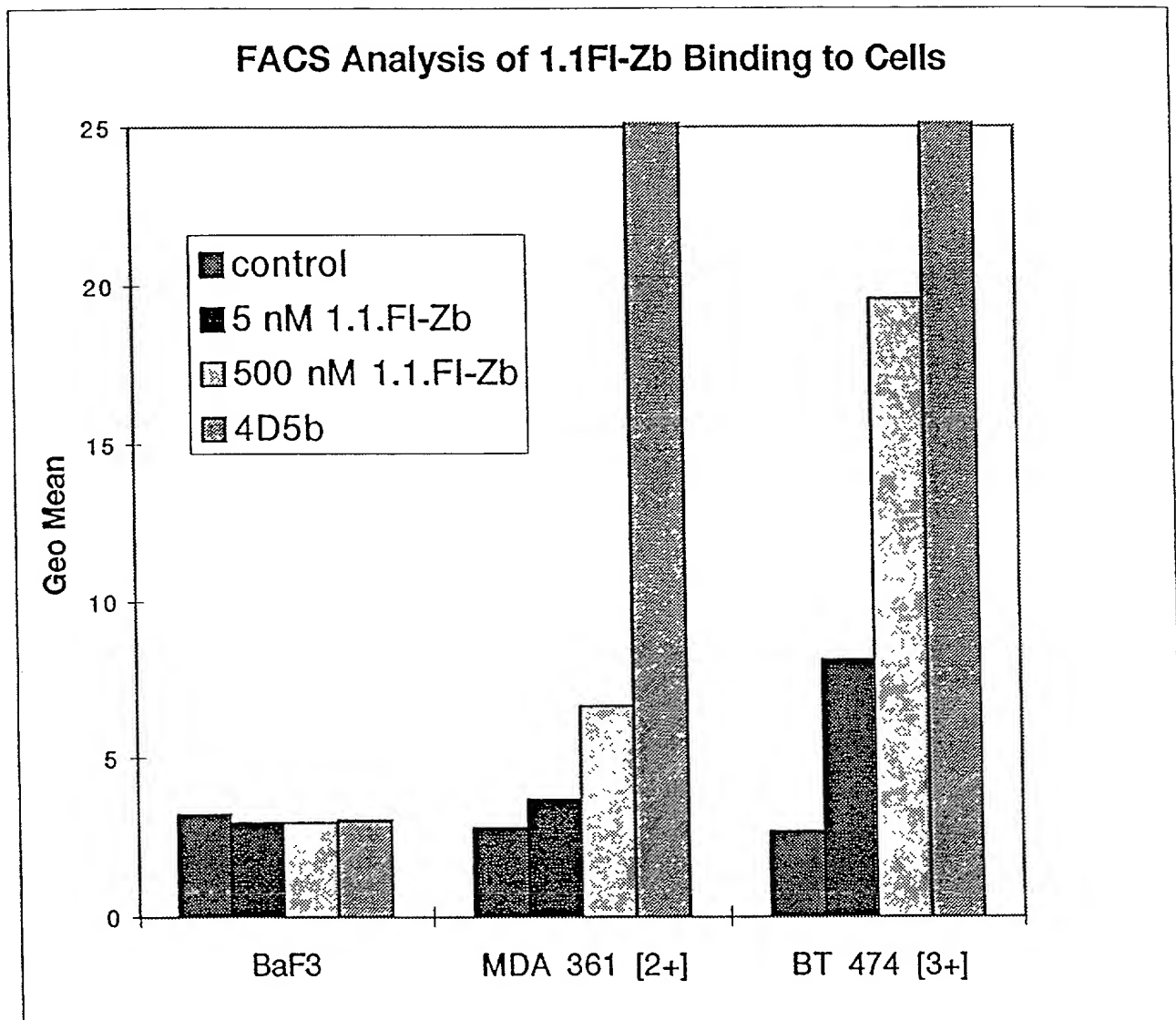
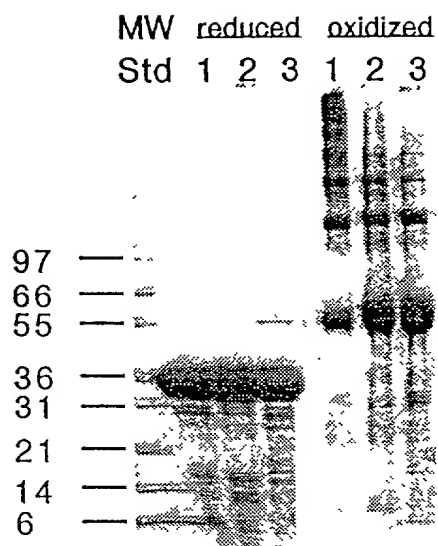


Figure 14



1 = Control Fc (no peptide fusion)  
2 = HER2-Fc fusion (l.lPI-Fc)

clone

Sequence

## Pool 1

1.1

Y E V E A W D C M G P G C A N L F E A H

## Library 1.1

1.1.8

1.1.9

1.1.10

1.1.1

1.1.2

1.1.6

1.1.11

1.1.3

1.1.4

1.1.5

1.1.7

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Y	E	G	E	S	W	G	C	I	G	P	G	C	A	S	L	F	D	A	H
Y	E	V	E	V	W	E	C	I	G	P	G	C	G	Y	L	F	G	A	H
Y	E	V	E	G	W	G	C	M	G	P	G	C	A	F	L	L	E	A	H
Y	S	F	E	G	W	G	C	I	G	P	G	C	A	Y	L	F	E	G	H
Y	D	F	E	G	W	G	C	I	G	P	G	C	G	N	L	L	E	A	H
Y	D	F	E	G	W	D	C	T	S	P	G	C	A	Y	L	F	E	G	H
D	E	V	E	S	W	G	C	I	G	P	G	C	A	Y	L	F	G	A	L
S	E	V	E	V	W	H	C	I	G	P	G	C	V	Y	L	F	E	A	Y
F	E	F	E	G	W	E	C	M	G	P	G	C	A	E	L	F	A	G	H
H	D	V	E	G	W	G	C	I	G	P	G	C	A	D	L	F	E	A	F

Consensus

Y E F E G W G C I G P G C A Y L F E A H

## Pool 7

7.1

C S W V L V Q C G G E W W H C C G L G C G L V V N A C

## Library 7.1

7.1.1

7.1.9

7.1.6

7.1.5

7.1.3

7.1.4

7.1.2

7.1.7

7.1.8

7.1.11

C	A	W	V	S	F	E	C	G	G	E	V	W	H	C	C	G	L	G	C	G	W	V	W	K	A	C
C	A	W	V	L	V	Q	C	G	G	E	W	W	H	C	C	G	P	G	G	E	F	V	V	D	A	C
C	A	W	V	A	Y	Y	C	G	G	E	L	W	H	C	C	G	P	G	G	F	V	V	D	S	C	
C	A	W	V	R	V	W	C	F	G	E	W	D	C	C	G	L	G	C	G	W	V	V	N	V	C	
C	A	W	V	R	V	L	C	G	G	E	W	W	H	C	C	G	L	G	C	G	W	V	V	E	A	C
C	S	W	V	S	V	L	C	G	G	E	W	W	Q	C	C	G	P	G	C	G	L	V	V	N	A	C
C	S	W	V	S	L	C	C	G	G	E	W	W	H	C	C	G	G	C	G	W	V	V	N	V	C	
C	S	W	V	L	L	H	C	G	G	E	W	W	H	C	C	G	G	C	G	W	V	G	E	A	C	
C	S	W	V	L	L	E	C	G	G	E	L	W	E	C	C	G	L	G	C	G	W	V	A	D	A	C
C	S	W	V	V	F	E	C	L	G	E	S	W	H	C	C	G	G	C	G	W	V	V	H	A	C	

Consensus

C A W V S V E C G G E W W H C C G P G C G W V V D A C



Figure 1c

**Pool 1**

1.1 Y E V E A W D C M G P G C A N L F E A H  
consensus Y E F E Q W Q C I G P G C A Y L F E A H

**Library 1.1.F**

- - - E - W Q C I G P G C - - L - - - -

1.1.FC	Y E W	E G	W G C I G P G C	P A	L G F G Y
1.1.FN	R W D	E E	W G C I G P G C	E W	L V V R K
1.1.FA	Q R N	E A	W G C I G P G C	E M	L C A W C
1.1.FM	L S P	E T	W G C I G P G C	E M	L C S W C
1.1.FE	E N W	E M	W G C I G P G C	K F	L C E P C
1.1.FH	C I D	E T	W G C I G P G C	E E	L R C K R
1.1.FB	T Q A	E R	W G C I G P G C	E C	L M S C V
1.1.FF	A P R	E V	W G C I G P G C	A C	L L R C I
1.1.FI	Q V Y	E S	W G C I G P G C	A C	L Q A C L
1.1.FK	R T E	E Q	W G C I G P G C	R C	L L S C L
1.1.FD	F A G	E S	W G C I G P G C	E C	L I G C L
1.1.FQ	T A R	E V	W G C I G P G C	N C	L A C L
1.1.FS	R P H	E P	W G C I G P G C	S C	L L S C I
1.1.FX	A S H	E V	W G C I G P G C	K C	L Q A C M
1.1.FY	K L N	E E	W G C I G P G C	A C	L L Q C W
1.1.FZ	K L N	E D	W G C I G P G C	A C	L L - C -

**Library 1.1.N**

E - W Q C I G P G C - - L - - - -

1.1.NC	E V	W G C I G P G C	K A	L C D W C
1.1.NB	E R	W G C I G P G C	R M	L C E W C
1.1.NM	E V	W G C I G P G C	D W	L C N W C
1.1.NQ	E V	W G C I G P G C	S M	L C G W C
1.1.NA	E V	W G C I G P G C	E C	L M N C L
1.1.NG	E G	W G C I G P G C	E C	L L R C L
1.1.NH	E G	W G C I G P G C	G C	L L K C L
1.1.NE	E P	W G C I G P G C	A C	L L G C L
1.1.NJ	E E	W G C I G P G C	A C	L L N C I
1.1.NF	E Q	W G C I G P G C	K C	L M G C L
1.1.NK	E Q	W G C I G P G C	G C	L L R C L
1.1.NR	E A	W G C I G P G C	S C	L M A C L

**Library 1.1.C**

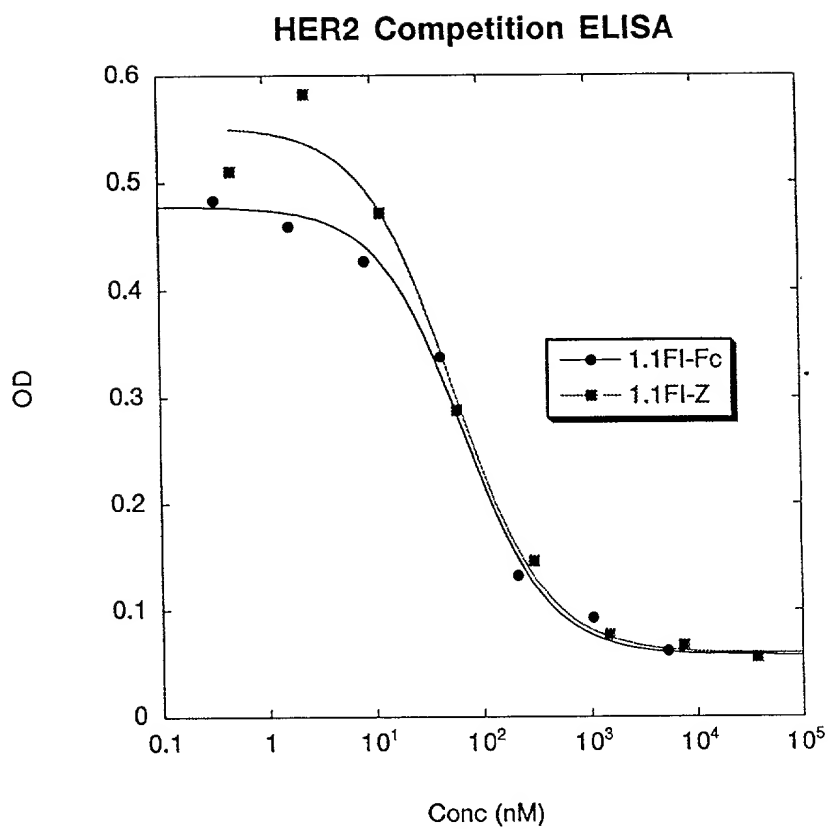
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1.1.CB	N W P	E G	W G C I G P G C	K L	L
1.1.CC	F N W	E K	W G C I G P G C	R T	L
1.1.CD	F S G	E R	W G C I G P G C	Q V	L
1.1.CE	G G W	E G	W G C I G P G C	R Y	L
1.1.CG	L W F	E R	W G C I G P G C	T -	L
1.1.CH	G I P	E G	W G C I G P G C	E W	L
1.1.CI	W W T	E R	W G C I G P G C	S M	L
1.1.CJ	- C -	E R	W G C I G P G C	S M	L
1.1.CL	L G W	E R	W G C I G P G C	R A	L
1.1.CM	S P W	E G	W G C I G P G C	R W	L
1.1.CP	R G W	E G	W G C I G P G C	S F	L

00609721-063000

Figure

17



**COMBINED DECLARATION FOR PATENT APPLICATION  
AND POWER OF ATTORNEY**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

**Compounds that Bind HER2**

the specification of which (check one) ☒ is attached hereto or ☐ was filed on  as Application Serial No.  and was amended on  (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate have a filing date before that of the application on which priority is claimed:

Prior Foreign Application(s):

Priority Claimed

Yes      No

Number	Country	Day/Month/Year Filed
I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional applications(s) listed below:		
50/142,232		2 July 1999
Application Ser. No.		Filing Date
I hereby claim the benefit under Title 35, United States Code, §120 of any United States applications(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56 which occurred between the filing date of the prior application and the national or PCT international filing date of this application:		
Application Ser. No.	Filing Date	Status: Patented, Pending, Abandoned
Application Ser. No.	Filing Date	Status: Patented, Pending, Abandoned

**POWER OF ATTORNEY:** As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Walter E. Buting - Reg. No. 23,092

Wendy M. Lee - Reg. No. 40,378

Elizabeth M. Barnes - Reg. No. 35,059

Richard B. Love - Reg. No. 34,659

Deirdre L. Conley - Reg. No. 36,487

Mark T. Kresnak - Reg. No. 42,767

Steven X. Cui - Reg. No. 44,637

Timothy R. Schwartz - Reg. No. 32,171

Janet E. Hasak - Reg. No. 28,616

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Sean A. Johnston - Reg. No. 35,910

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Dennis G. Kleid - Reg. No. 32,037

Jeffrey S. Kubinec - Reg. No. 36,575

Send correspondence to Genentech, Inc.

Attn: Jeffrey S. Kubinec  
1 DNA Way  
South San Francisco, CA 94080  
Telephone: (650) 225-8228

I hereby declare that all statements made herein of my own knowledge and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both, under Section 1001 of Title 18 of the United States Code and that willful false statements may jeopardize the validity of the application or any patent issued thereon.

The undersigned hereby authorizes the U.S. attorney or agent named herein to accept and follow instructions from his foreign patent agent as to any action to be taken in the Patent and Trademark Office regarding this application without direct communication between the U.S. attorney or agent and the undersigned. In the event of a change in the persons from whom instructions may be taken, the U.S. attorney or agent named herein will be so notified by the undersigned.

Full name of sole or first inventor

Mark S. Dennis

Inventor's signature



Date

6-26-00

Residence

120 Plymouth, San Carlos, California 94070

Citizenship

United States

Post Office Address

1 DNA Way

South San Francisco, CA 94080

# Sequence Listing

<110> Mark S. Dennis

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<151> 1999-07-02

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Leu	Cys	Ala	Trp	Cys
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Leu	Cys	Ser	Trp	Cys
				20

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Trp Cys

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Trp Cys

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Trp Cys

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20

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Leu Leu Ser Cys Ile  
20

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Cys Leu

<210> 20

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Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Glu Cys Leu Leu Arg  
1 5 10 15

Cys Leu

<210> 21

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 21

Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Gly Cys Leu Leu Lys  
1 5 10 15

Cys Leu

<210> 22  
<211> 17  
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<213> Artificial Sequence

<220>  
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<400> 22  
Glu Pro Trp Gly Cys Ile Gly Pro Gly Cys Ala Cys Leu Leu Gly  
1 5 10 15

Cys Leu

<210> 23  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 23  
Glu Glu Trp Gly Cys Ile Gly Pro Gly Cys Ala Cys Leu Leu Asn  
1 5 10 15

Cys Ile

<210> 24  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 24  
Glu Gln Trp Gly Cys Ile Gly Pro Gly Cys Lys Cys Leu Met Gly  
1 5 10 15

Cys Leu

<210> 25  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 25  
Glu Gln Trp Gly Cys Ile Gly Pro Gly Cys Gly Cys Leu Leu Arg  
1 5 10 15

Cys Leu

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Cys Leu

Leu Leu Xaa Cys Leu  
20

Leu Cys

8



<220>

<223> synthetic peptide sequence

<400> 33

Asn Trp Pro Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Lys Leu  
1 5 10 15

Leu

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 34

Phe Asn Trp Glu Lys Trp Gly Cys Ile Gly Pro Gly Cys Arg Thr  
1 5 10 15

Leu

<210> 35

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

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<400> 35

Phe Ser Gly Glu Arg Trp Gly Cys Ile Gly Pro Gly Cys Gln Val  
1 5 10 15

Leu

<210> 36

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

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<400> 36

Gly Gly Trp Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Arg Tyr  
1 5 10 15

Leu

<210> 37  
<211> 16  
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<213> Artificial Sequence

<220>  
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<220>  
<221> unsure  
<222> 15  
<223> unknown amino acid

<400> 37  
Leu Trp Phe Glu Arg Trp Gly Cys Ile Gly Pro Gly Cys Thr Xaa  
1 5 10 15

Leu

<210> 38  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 38  
Gly Ile Pro Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Glu Trp  
1 5 10 15

Leu

<210> 39  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 39  
Trp Trp Thr Glu Arg Trp Gly Cys Ile Gly Pro Gly Cys Ser Met  
1 5 10 15

Leu

<210> 40  
<211> 20  
<212> PRT  
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<220>  
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<220>  
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<222> 1, 3, 17-20  
<223> unknown amino acid

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Xaa Cys Xaa Glu Arg Trp Gly Cys Ile Gly Pro Gly Cys Ser Met  
1 5 10 15  
Leu Xaa Xaa Xaa Xaa  
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<210> 41  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 41  
Leu Gly Trp Glu Arg Trp Gly Cys Ile Gly Pro Gly Cys Arg Ala  
1 5 10 15  
Leu

<210> 42  
<211> 16  
<212> PRT  
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<220>  
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<400> 42  
Ser Pro Trp Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Arg Trp  
1 5 10 15  
Leu

<210> 43  
<211> 16  
<212> PRT  
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<220>  
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<400> 43  
Arg Gly Trp Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Ser Phe  
1 5 10 15  
Leu



<210> 44  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
 <221> unsure  
 <222> 1-2, 5, 14-15, 17-20  
 <223> unknown amino acid

<400> 44  
 Xaa Xaa Trp Glu Xaa Trp Gly Cys Ile Gly Pro Gly Cys Xaa Xaa  
     1                    5                    10                    15  
 Leu Xaa Xaa Xaa Xaa  
                     20

<210> 45  
 <211> 27  
 <212> PRT  
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<220>  
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<400> 45  
 Cys Ser Trp Val Leu Val Gln Cys Gly Gly Glu Trp Trp His Cys  
     1                    5                    10                    15  
 Cys Gly Leu Gly Cys Gly Leu Val Val Asn Ala Cys  
                     20                    25

<210> 46  
 <211> 27  
 <212> PRT  
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<220>  
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<400> 46  
 Cys Ala Trp Val Ser Phe Glu Cys Gly Gly Glu Val Trp His Cys  
     1                    5                    10                    15  
 Cys Gly Leu Gly Cys Gly Trp Val Trp Lys Ala Cys  
                     20                    25

<210> 47  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic peptide sequence

<400> 47  
Cys Ala Trp Val Leu Val Gln Cys Gly Gly Glu Trp Trp His Cys  
1 5 10 15

Cys Gly Pro Gly Cys Glu Phe Val Val Asp Ala Cys  
20 25

<210> 48  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 48  
Cys Ala Trp Val Ala Val Tyr Cys Gly Gly Glu Leu Trp His Cys  
1 5 10 15

Cys Gly Pro Gly Cys Gly Phe Val Val Asp Ser Cys  
20 25

<210> 49  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 49  
Cys Ala Trp Val Arg Val Trp Cys Phe Gly Glu Trp Trp Asp Cys  
1 5 10 15

Cys Gly Leu Gly Cys Gly Trp Val Val Asn Val Cys  
20 25

<210> 50  
<211> 27  
<212> PRT  
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<220>  
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<400> 50  
Cys Ala Trp Val Arg Val Leu Cys Gly Gly Glu Trp Trp His Cys  
1 5 10 15

Cys Gly Leu Gly Cys Gly Trp Val Val Glu Ala Cys  
20 25

<210> 51  
<211> 27  
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<220>  
<223> synthetic peptide sequence

<400> 51  
Cys Ser Trp Val Ser Val Leu Cys Gly Gly Glu Trp Trp Gln Cys  
1 5 10 15  
Cys Gly Pro Gly Cys Gly Leu Val Val Asn Ala Cys  
20 25

<210> 52  
<211> 27  
<212> PRT  
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<220>  
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<400> 52  
Cys Ser Trp Val Ser Leu Gln Cys Gly Gly Glu Trp Trp His Cys  
1 5 10 15  
Cys Gly Gly Gly Cys Gly Trp Val Val Asn Val Cys  
20 25

<210> 53  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 53  
Cys Ser Trp Val Leu Leu His Cys Gly Gly Glu Trp Trp His Cys  
1 5 10 15  
Cys Gly Gly Gly Cys Gly Trp Val Gly Glu Ala Cys  
20 25

<210> 54  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 54  
Cys Ser Trp Val Leu Leu Glu Cys Gly Gly Glu Leu Trp Glu Cys  
1 5 10 15  
Cys Gly Leu Gly Cys Gly Trp Val Ala Asp Ala Cys  
20 25

<210> 55  
<211> 27  
<212> PRT  
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<220>  
<223> synthetic peptide sequence

<400> 55  
Cys Ser Trp Val Val Phe Glu Cys Leu Gly Glu Ser Trp His Cys  
1 5 10 15  
Cys Gly Gly Gly Cys Gly Trp Val Val His Ala Cys  
20 25

<210> 56  
<211> 27  
<212> PRT  
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<400> 56  
Cys Ala Trp Val Ser Val Glu Cys Gly Gly Glu Trp Trp His Cys  
1 5 10 15  
Cys Gly Pro Gly Cys Gly Trp Val Val Asp Ala Cys  
20 25

<210> 57  
<211> 20  
<212> PRT  
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<220>  
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<400> 57  
Tyr Glu Val Glu Ala Trp Asp Cys Met Gly Pro Gly Cys Ala Asn  
1 5 10 15  
Leu Phe Glu Ala His  
20

<210> 58  
<211> 20  
<212> PRT  
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<220>  
<223> synthetic peptide sequence

<400> 58  
Tyr Glu Phe Glu Gly Trp Asp Cys Met Gly Pro Gly Cys Ala Ser  
1 5 10 15

Val Phe Gly Ala His  
20

<210> 59  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 59  
Tyr Glu Gly Glu Ser Trp Gly Cys Ile Gly Pro Gly Cys Ala Ser  
1 5 10 15

Leu Phe Asp Ala His  
20

<210> 60  
<211> 20  
<212> PRT  
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<220>  
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<400> 60  
Tyr Glu Val Glu Val Trp Glu Cys Ile Gly Pro Gly Cys Gly Tyr  
1 5 10 15

Leu Phe Gly Ala His  
20

<210> 61  
<211> 20  
<212> PRT  
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<220>  
<223> synthetic peptide sequence

<400> 61  
Tyr Glu Val Glu Gly Trp Gly Cys Met Gly Pro Gly Cys Ala Phe  
1 5 10 15

Leu Leu Glu Ala His  
20

<210> 62  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 62

Tyr Ser Phe Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Ala Tyr  
1 5 10 15

Leu Phe Glu Gly His  
20

<210> 63

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 63

Tyr Asp Phe Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Gly Asn  
1 5 10 15

Leu Leu Glu Ala His  
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<210> 64

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 64

Tyr Asp Phe Glu Gly Trp Asp Cys Thr Gly Pro Gly Cys Ala Tyr  
1 5 10 15

Leu Phe Glu Gly His  
20

<210> 65

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 65

Asp Glu Val Glu Ser Trp Gly Cys Ile Gly Pro Gly Cys Ala Tyr  
1 5 10 15

Leu Phe Gly Ala Leu  
20

<210> 66

<211> 20

<212> PRT

<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 66  
Ser Glu Val Glu Val Trp His Cys Ile Gly Pro Gly Cys Val Tyr  
1 5 10 15

Leu Phe Glu Ala Tyr  
20

<210> 67  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 67  
Phe Glu Phe Glu Gly Trp Glu Cys Met Gly Pro Gly Cys Ala Glu  
1 5 10 15

Leu Phe Ala Gly His  
20

<210> 68  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 68  
His Asp Val Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Ala Asp  
1 5 10 15

Leu Phe Glu Ala Phe  
20

<210> 69  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide sequence

<400> 69  
Tyr Glu Phe Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Ala Tyr  
1 5 10 15

Leu Phe Glu Ala His  
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<210> 70  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
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 <220>  
 <221> Mutagen  
 <222> 2-7, 9-14, 17-19, 21-26  
 <223> More than one possible amino acid  
  
 <400> 70  
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 1 5 10 15  
 Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 20 25

<210> 71  
 <211> 6  
 <212> PRT  
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 <220>  
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<220>  
 <221> Mutagen  
 <222> 2  
 <223> Xaa can be Cys or Ile

<400> 71  
 Cys Xaa Gly Pro Gly Cys  
 1 5

<210> 72  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
 1 5 10 15  
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 20 25 30  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys  
 35 40 45  
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 50 55 60  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
 65 70 75



Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 80 85 90  
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 95 100 105  
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 110 115 120  
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 125 130 135  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 140 145 150  
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 155 160 165  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 170 175 180  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 185 190 195  
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 200 205 210  
 Ser Leu Ser Leu Ser Pro Gly Lys  
 215

<210> 73  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 73  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
 1 5 10 15  
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 20 25 30  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys  
 35 40 45  
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 50 55 60  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser  
 65 70 75  
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 80 85 90  
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 95 100 105

Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
				110					115					120	
Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	
				125					130					135	
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	
				140					145					150	
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	
				155					160					165	
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	
				170					175					180	
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	
				185					190					195	
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	
				200					205					210	
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
				215											

<210> 74  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 74

Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
1				5					10					15	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	
				20					25					30	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	
				35					40					45	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	
				50					55					60	
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	
				65					70					75	
Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	
				80					85					90	
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	
				95					100					105	
Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
				110					115					120	
Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	
				125					130					135	

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 140 145 150  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
 155 160 165  
 Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 170 175 180  
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 185 190 195  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 200 205 210  
 Leu Ser Leu Ser Pro Gly Lys  
 215

<210> 75  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 75  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
 1 5 10 15  
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 20 25 30  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln  
 35 40 45  
 Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 50 55 60  
 Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser  
 65 70 75  
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 80 85 90  
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 95 100 105  
 Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 110 115 120  
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
 125 130 135  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
 140 145 150  
 Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr  
 155 160 165

Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys
				170					175					180
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Ile	Phe	Ser
				185					190					195
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	Arg	Phe	Thr	Gln	Lys
				200					205					210
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
				215										

<210> 76  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 76

Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
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Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				20					25					30
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln
				35					40					45
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
				50					55					60
Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
				65					70					75
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
				80					85					90
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys
				95					100					105
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
				110					115					120
Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser
				125					130					135
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
				140					145					150
Glu	Trp	Glx	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
				155					160					165
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg
				170					175					180
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser
				185					190					195



<210> 78  
 <211> 218  
 <212> PRT  
 <213> Mus musculus

<400> 78

Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro
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Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val
				20					25					30
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln
				35					40					45
Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr
				50					55					60
Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser
				65					70					75
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe
				80					85					90
Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg
				95					100					105
Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr
				110					115					120
Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr
				125					130					135
Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	Tyr	Val
				140					145					150
Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	Thr
				155					160					165
Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys
				170					175					180
Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser
				185					190					195
Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys
				200					205					210
Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys							
				215										

<210> 79  
 <211> 218  
 <212> PRT  
 <213> Mus musculus

1. The first group of people who are interested in the study of the history of the United States are the people who are interested in the history of the United States.

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<210> 80
<211> 218
<212> PRT
<213> Mus musculus
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Pro	Pro	Gly	Asn	Ile	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro
1				5					10					15
Pro	Lys	Pro	Lys	Asp	Ala	Leu	Met	Ile	Ser	Leu	Thr	Pro	Lys	Val
				20					25					30

Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	His	35	40	45
Val	Ser	Trp	Phe	Val	Asp	Asn	Lys	Glu	Val	His	Thr	Ala	Trp	Thr	50	55	60
Gln	Pro	Arg	Glu	Ala	Gln	Tyr	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	65	70	75
Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Arg	Gly	Lys	Glu	Phe	80	85	90
Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Arg	95	100	105
Thr	Ile	Ser	Lys	Pro	Lys	Gly	Arg	Ala	Gln	Thr	Pro	Gln	Val	Tyr	110	115	120
Thr	Ile	Pro	Pro	Pro	Arg	Glu	Gln	Met	Ser	Lys	Lys	Lys	Val	Ser	125	130	135
Leu	Thr	Cys	Leu	Val	Thr	Asn	Phe	Phe	Ser	Glu	Ala	Ile	Ser	Val	140	145	150
Glu	Trp	Glu	Arg	Asn	Gly	Glu	Leu	Glu	Gln	Asp	Tyr	Lys	Asn	Thr	155	160	165
Pro	Pro	Ile	Leu	Asp	Ser	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser	Lys	170	175	180
Leu	Thr	Val	Asp	Thr	Asp	Ser	Trp	Leu	Gln	Gly	Glu	Ile	Phe	Thr	185	190	195
Cys	Ser	Val	Val	His	Glu	Ala	Leu	His	Asn	His	His	Thr	Gln	Lys	200	205	210
Asn	Leu	Ser	Arg	Ser	Pro	Gly	Lys								215		

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<211> 20

<212> PRT

<213> Artificial Sequence

<220>

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<400> 81

Gln	Val	Tyr	Glu	Ser	Trp	Gly	Cys	Ile	Gly	Pro	Gly	Cys	Ala	Cys	1	5	10	15
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Leu	Gln	Ala	Cys	Leu	20
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<211> 46

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<220>

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<400> 82

Gln Val Tyr Glu Ser Trp Gly Cys Ile Gly Pro Gly Cys Ala Cys  
1 5 10 15

Leu Gln Ala Cys Leu Gly Gly Gly Ser Gly Gly Gln Val Tyr Glu  
20 25 30

Ser Trp Gly Cys Ile Gly Pro Gly Cys Ala Cys Leu Gln Ala Cys  
35 40 45

Leu

<210> 83

<211> 27

<212> PRT

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<220>

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<400> 83

Cys Ala Trp Val Ser Val Glu Cys Gly Gly Glu Trp Trp His Cys  
1 5 10 15

Cys Gly Pro Gly Cys Gly Trp Val Val Asp Ala Cys  
20 25

<210> 84

<211> 20

<212> PRT

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<400> 84

Tyr Ser Phe Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Ala Tyr  
1 5 10 15

Leu Phe Glu Gly His  
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<210> 85

<211> 20

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<220>

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<400> 85

Tyr Glu Trp Glu Gly Trp Gly Cys Ile Gly Pro Gly Cys Pro Ala  
1 5 10 15

Leu Gly Phe Gly Tyr  
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<210> 86  
<211> 20  
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<400> 86  
Gln Arg Asn Glu Ala Trp Gly Cys Ile Gly Pro Gly Cys Glu Met  
1 5 10 15

Leu Cys Ala Trp Cys  
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<210> 87  
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<400> 87  
Thr Gln Ala Glu Arg Trp Gly Cys Ile Gly Pro Gly Cys Glu Cys  
1 5 10 15

Leu Met Ser Cys Val  
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<210> 88  
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<400> 88  
Cys Ile Asp Glu Thr Trp Gly Cys Ile Gly Pro Gly Cys Glu Glu  
1 5 10 15

Leu Arg Cys Lys Arg  
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<211> 17  
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 Asn Val Cys Glu Phe Trp Gly Cys Ile Gly Pro Gly Cys Ala Gln  
 1 5 10 15

Leu Cys

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 <211> 27  
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<220>  
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 <222> 1-14, 16, 21-27  
 <223> More than one possible amino acid

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 1 5 10 15  
 Xaa Gly Pro Gly Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25

<210> 91  
 <211> 20  
 <212> PRT  
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<220>  
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 <222> 1-3, 5, 14-15, 17-20  
 <223> More than one possible amino acid

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 1 5 10 15  
 Leu Xaa Xaa Xaa Xaa  
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<210> 92  
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 <222> 1-7, 9, 14-20  
 <223> More than one possible amino acid  
  
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 1 5 10 15  
  
 Xaa Xaa Xaa Xaa Xaa  
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 <222> 1-5, 7, 9, 14-20  
 <223> More than one possible amino acid  
  
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 1 5 10 15  
  
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<210> 101  
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<210> 102  
<211> 4  
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<210> 103  
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<220>  
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<210> 104  
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<210> 105  
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<210> 106  
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<210> 107  
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<210> 120  
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<210> 122  
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<400> 122  
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<210> 123  
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<400> 123  
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<210> 124  
 <211> 4  
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<220>  
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<400> 124  
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<210> 125  
 <211> 27  
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<220>  
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<220>  
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 <222> 2-7, 9-14, 17-19, 21-26  
 <223> More than one possible amino acid

<400> 125  
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 1 5 10 15  
 Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 20 25

<210> 126  
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<220>  
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<220>  
 <221> Mutagen  
 <222> 1-10, 12, 14, 21-27  
 <223> More than one possible amino acid

<400> 126  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Trp Xaa Cys  
 1 5 10 15  
 Cys Gly Pro Gly Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25

<210> 127  
 <211> 10  
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 <221> Mutagen  
 <222> 2, 5-7, 9  
 <223> More than one possible amino acid  
  
 <400> 127  
 Cys Xaa Trp Val Xaa Xaa Xaa Cys Xaa Gly  
   1                  5                  10

<210> 128  
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<220>  
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<220>  
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 <222> 6-7  
 <223> More than one possible amino acid

<400> 128  
 Cys Ala Trp Val Leu Xaa Xaa Cys Gly Gly  
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<210> 129  
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<400> 129  
 Gly Gly Gly Ser Gly Gly  
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<210> 130  
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<210> 131  
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<220>  
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<400> 131

Gly Gly Gly Arg Gly Gly  
1 5

<210> 132

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

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<400> 132

Tyr Glu Val Glu Ala Trp Asp Cys Met Gly Pro Gly Cys Ala Asn  
1 5 10 15

Leu Phe Glu Ala His  
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<210> 133

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 133

Ser Ser Glu Cys Ala Cys Asp Lys Gly Gly Arg Arg Val Leu Cys  
1 5 10 15

Ile Asn Lys Val Gly  
20

<210> 134

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 134

Glu Pro His Gly Cys Ser Leu Trp Asp Trp Glu Leu Arg Thr Cys  
1 5 10 15

Ser Glu Tyr Ala Asn  
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<210> 135

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide sequence

<400> 135  
Lys Glu Arg Pro Cys Ala Gly Asp Ala Pro Arg Lys Gly Val Cys  
1 5 10 15

His Val Ala Thr His  
20

<210> 136  
<211> 20  
<212> PRT  
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<223> synthetic peptide sequence

<400> 136  
Lys Val Arg Ser Cys Ile Glu Glu Ser Leu Asp Thr Arg Arg Cys  
1 5 10 15

Tyr Leu Val Val Glu  
20

<210> 137  
<211> 20  
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<400> 137  
Ala Lys Thr Ser Ser Cys Gly Glu His Glu Glu Arg Arg Ala Val  
1 5 10 15

Cys Val Leu Ser Arg  
20

<210> 138  
<211> 8  
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<400> 138  
Lys Val Trp Ser Val Gln Ser Pro  
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<210> 139  
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 Gly Lys Val Gln Arg Cys Ile Pro  
 1 5

<210> 140  
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<210> 141  
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<210> 142  
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<220>  
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<210> 143  
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 Thr Ser Cys Arg Arg Val Phe Cys Ala Val  
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<210> 144  
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1 5

<210> 145  
<211> 10  
<212> PRT  
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<400> 145  
Lys Val Cys Thr Arg Val Cys Cys Gly Thr  
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<210> 146  
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<400> 146  
His Pro Cys His Met Arg Val Leu Cys Ala Ala  
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<210> 147  
<211> 13  
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<400> 147  
Arg Gly Cys Lys Ala Thr Gly Lys Val Leu Cys Ser Leu  
1 5 10

<210> 148  
<211> 12  
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<400> 148  
Ser Gly Cys Leu Arg Ala Val Gly Ala Cys Asn Thr  
1 5 10



<210> 149  
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 1 5 10  
  
 <210> 151  
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 Lys Val Cys His Ala Ser Ser Gly Cys Val Ala  
 1 5 10  
  
 <210> 152  
 <211> 11  
 <212> PRT  
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 Arg Ala Cys Gln Arg Ala Cys Leu Cys Pro Ala  
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 <212> PRT  
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<400> 153  
 Arg Ser Cys Ala Asp Val Ala Ser Arg Cys Trp Glu His Cys Ile  
           1                  5                  10                  15

Thr

<210> 154  
 <211> 16  
 <212> PRT  
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<220>  
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<400> 154  
 Thr Asp Cys Gly Arg Val Ala Ser Val Cys Trp Glu Ser Cys Leu  
           1                  5                  10                  15

Ile

<210> 155  
 <211> 19  
 <212> PRT  
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<220>  
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<400> 155  
 Cys Cys Glu Thr Arg Trp Trp Cys Gln Trp Gly Phe Cys Ser Gly  
           1                  5                  10                  15

Ser Ala Cys Cys

<210> 156  
 <211> 12  
 <212> PRT  
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<220>  
 <223> synthetic peptide sequence

<400> 156  
 Gly Cys Lys Arg Val Cys Ser Leu Gly Val Met Cys  
           1                  5                  10

<210> 157  
 <211> 27  
 <212> PRT  
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<220>  
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<400> 157  
 Cys Ser Trp Val Leu Val Gln Cys Gly Gly Glu Trp Trp His Cys  
           1                  5                  10                  15

Cys Gly Leu Gly Cys Gly Leu Val Val Asn Ala Cys  
                   20                  25

<210> 158  
 <211> 21  
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<220>  
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 Cys Gly Cys Glu Glu Arg Lys Ala Trp Lys Cys Gln Glu Ala Cys  
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Ala Arg Ser Gly Thr Val  
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<210> 159  
 <211> 84  
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<220>  
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<400> 159  
 cgcgcccagg tgtacgagtc ctggggatgc atcgggccccg gctgcgcctg 50  
 cctgcaggcc tgcctgggag gcgggagctc cggc 84

<210> 160  
 <211> 80  
 <212> DNA  
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<220>  
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<400> 160  
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 cgatgcatcc ccaggactcg tacacctggg 80

<210> 161  
 <211> 20  
 <212> PRT  
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<220>  
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<220>

<221> Mutagen

<222> 1-7, 14-20

<223> More than one possible amino acid

<400> 161

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Ile Gly Pro Gly Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa  
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<210> 162

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

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<220>

<221> Mutagen

<222> 6-7

<223> More than one possible amino acid

<400> 162

Cys Ser Trp Val Leu Xaa Xaa Cys Gly Gly  
1 5 10